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Date of mailing (day/month/year) 16 March 2000 (16.03.00)	
International application No. PCT/EP98/05542	**Applicant's or agent's file reference** 18397P WO
International filing date (day/month/year) 01 September 1998 (01.09.98)	**Priority date** (day/month/year) 06 July 1998 (06.07.98)
Applicant HEILBRONN, Regine et al	

1. The designated Office is hereby notified of its election made:

[X] in the demand filed with the International Preliminary Examining Authority on:
04 February 2000 (04.02.00)

[ ] in a notice effecting later election filed with the International Bureau on:

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C.(suite) DOCUMENTS CONSIDERES COMME PERTINENTS

Catégorie *	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
X	VIROLOGY, vol.134, no.1, 15 Avril 1984 pages 64 - 71 GEORG-FRIES, B. ET AL. 'Analysis of proteins, helper dependence and seroepidemiology of a new human parvovirus' voir page 68, ligne 17 - ligne 22	1-4,16
X	JOURNAL OF GENERAL VIROLOGY, vol.67, no.1, Janvier 1986 pages 181 - 185 BAUER, H.J. & MONREAL, G 'Herpesviruses provide helper functions for avian adeno-associated parvovirus' voir le document en entier	1-4,16
X	JOURNAL OF VIROLOGICAL METHODS, vol.29, no.3, Septembre 1990 pages 335 - 340 BAUER, A. ET AL. 'Growth of avian adeno-associated virus in chicken cells transfected with fowl adenovirus serotype 1 DNA' voir le document en entier	1-5,16
X	EP,A,0 488 528 (APPLIED IMMUNESCIENCES) 3 Juin 1992 cité dans la demande voir revendications 7,9; exemple 5	1,2, 10-12, 14,16, 17,19,20
X	US,A,5 139 941 (MUZYCZKA, N. ET AL.) 18 Août 1992 voir le document en entier	1-3
X	WO,A,91 18088 (THE UNITED STATES OF AMERICA, US DEPARTMENT OF COMMERCE) 28 Novembre 1991 cité dans la demande voir page 24, ligne 35 - page 25, ligne 24	1,2,16
X	JOURNAL OF CELLULAR BIOCHEMISTRY, vol.SUP, no.18A, 4 Janvier 1994 page 214 CARTER, T. ET AL. 'Adeno-associated virus vectors for in vivo gene transfer' * résumé DZ 001 *	1,2
O,X	& Keystone symposium on gene therapy Copper mountain, USA 15-22 Janvier 1994	1,2

-/--

RAPPORT DE RECHERCHE INTERNATIONALE

Renseignements relatifs aux me[illegible]le familles de brevets

[illegible]ternationale No
[illegible]/FR 95/00054

Document brevet cité au rapport de recherche	Date de publication	Membre(s) de la famille de brevet(s)		Date de publication
EP-A-0488528	03-06-92	US-A-	5173414	22-12-92
		CA-A-	2054517	01-05-92
		JP-A-	5308975	22-11-93
		US-A-	5354678	11-10-94
US-A-5139941	18-08-92	AUCUN		
WO-A-9118088	28-11-91	AU-A-	7906691	10-12-91

C.(suite) DOCUMENTS CONSIDERES COMME PERTINENTS

Catégorie *	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA., vol.81, no.20, Octobre 1984, WASHINGTON US pages 6466 - 6470 HERMONAT, P. L. & MUZYCZKA, N. 'Use of adeno-associated virus as a mammalian DNA cloning vector: transduction of neomycin resistance into mammlian tissue culture cells' voir page 70, ligne 1, alinéa IV	1,2,16

C.(Fortsetzung) ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie*	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
X	WO 95 20671 A (RHONE POULENC RORER SA ;DESCAMPS VINCENT (FR); PERRICAUDET MICHEL) 3. August 1995 siehe Zusammenfassung; Ansprüche 1,4,15 siehe Seite 3, Zeile 25 - Zeile 30 siehe Seite 7, Zeile 17 - Zeile 24 ---	1,4,7,8, 10, 14-16, 18,22; 23,25,28
A	RIXON F J AND MCLAUCHLAN: "Insertion of DNA sequences at a unique restriction enzyme site engineered for vector purposes into the genome of herpes simplex virus type 1" JOURNAL OF GENERAL VIROLOGY, Bd. 113, Nr. 71, 1. Januar 1990, Seite 2931 2939 XP002079295 in der Anmeldung erwähnt siehe Zusammenfassung siehe Seite 2932, linke Spalte siehe Seite 2935, linke Spalte ---	3,6,12, 27
A	SRIVASTAVA A ET AL: "NUCLEOTIDE SEQUENCE AND ORGANIZATION OF THE ADENO-ASSOCIATED VIRUS 2 GENOME" JOURNAL OF VIROLOGY, Bd. 45, Nr. 2, 1. Februar 1983, Seiten 555-564, XP002058633 in der Anmeldung erwähnt ---	
A	CONWAY ET AL.: "Recombinant adeno-associated virus type 2 replication and packaging is entirely supported by herpes simplex virus type 1 amplicon expressing rep and cap" JOURNAL OF VIROLOGY, Bd. 71, Nr. 11, November 1997, Seiten 8780-8789, XP002102271 in der Anmeldung erwähnt siehe Zusammenfassung -----	1,4

RAPPORT DE RECHERCHE INTERNATIONALE

nd rnationale No
i/FR 95/00054

A. CLASSEMENT DE L'OBJET DE LA DEMANDE
CIB 6 C12N15/86 C12N15/35 C12N15/27 C12N5/10 C12N7/01

Selon la classification internationale des brevets (CIB) ou à la fois selon la classification nationale et la CIB

B. DOMAINES SUR LESQUELS LA RECHERCHE A PORTE

Documentation minimale consultée (système de classification suivi des symboles de classement)
CIB 6 C12N C07K

Documentation consultée autre que la documentation minimale dans la mesure où ces documents relèvent des domaines sur lesquels a porté la recherche

Base de données électronique consultée au cours de la recherche internationale (nom de la base de données, et si cela est réalisable, termes de recherche utilisés)

C. DOCUMENTS CONSIDERES COMME PERTINENTS

Catégorie *	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
X	VIROLOGY, vol.152, no.1, 15 Juillet 1986 pages 110 - 117 SCHLEHOFER, J.R. ET AL. 'Vaccinia Virus, Herpes Simplex Virus and carcinogens induce DNA amplification in a human cell line and support replication of a helper dependent parvovirus' voir page 115, ligne 5 - ligne 15; figure 7 --- -/--	1-4,16

[X] Voir la suite du cadre C pour la fin de la liste des documents

[X] Les documents de familles de brevets sont indiqués en annexe

* Catégories spéciales de documents cités:

"A" document définissant l'état général de la technique, non considéré comme particulièrement pertinent

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"&" document qui fait partie de la même famille de brevets

Date à laquelle la recherche internationale a été effectivement achevée	Date d'expédition du présent rapport de recherche internationale
5 Avril 1995	02.05.1995

Nom et adresse postale de l'administration chargée de la recherche internationale	Fonctionnaire autorisé
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INTERNATIONA[L] RECHERCHENBERICHT

[...ken] [...iales] Aktenzeichen
PCT/EP 98/05542

A. KLASSIFIZIERUNG DES ANMELDUNGSGEGENSTANDES
IPK 6 C12N15/86 C12N7/01 C12N7/04 C12N5/10

Nach der Internationalen Patentklassifikation (IPK) oder nach der nationalen Klassifikation und der IPK

B. RECHERCHIERTE GEBIETE

Recherchierter Mindestprüfstoff (Klassifikationssystem und Klassifikationssymbole)
IPK 6 C12N

Recherchierte aber nicht zum Mindestprüfstoff gehörende Veröffentlichungen, soweit diese unter die recherchierten Gebiete fallen

Während der internationalen Recherche konsultierte elektronische Datenbank (Name der Datenbank und evtl. verwendete Suchbegriffe)

C. ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie°	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
X	WO 95 06743 A (UAB RESEARCH FOUNDATION) 9. März 1995 in der Anmeldung erwähnt siehe Zusammenfassung; Ansprüche 1,5,7,15,19,23,30,35; Beispiele VI,VII siehe Seite 6, Zeile 4 - Seite 7, Zeile 20 siehe Seite 10, Zeile 20 - Seite 11, Zeile 30 siehe Seite 12, Zeile 29 - Seite 13, Zeile 13 siehe Seite 15, Zeile 18 - Zeile 28 --- -/--	1,2,4,5, 7,9-21, 23-28

[X] Weitere Veröffentlichungen sind der Fortsetzung von Feld C zu entnehmen

[X] Siehe Anhang Patentfamilie

° Besondere Kategorien von angegebenen Veröffentlichungen :

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"&" Veröffentlichung, die Mitglied derselben Patentfamilie ist

Datum des Abschlusses der internationalen Recherche	Absendedatum des internationalen Recherchenberichts
10. Mai 1999	28/05/1999

Name und Postanschrift der Internationalen Recherchenbehörde	Bevollmächtigter Bediensteter
Europäisches Patentamt, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Ceder, O

INTERNATIONAL SEARCH REPORT

International Application No
T/FR 95/00054

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JOURNAL OF GENERAL VIROLOGY, vol.67, no.1, January 1986 pages 181 - 185 BAUER, H.J. & MONREAL, G 'Herpesviruses provide helper functions for avian adeno-associated parvovirus' see the whole document	1-4,16
X	JOURNAL OF VIROLOGICAL METHODS, vol.29, no.3, September 1990 pages 335 - 340 BAUER, A. ET AL. 'Growth of avian adeno-associated virus in chicken cells transfected with fowl adenovirus serotype 1 DNA' see the whole document	1-5,16
X	EP,A,0 488 528 (APPLIED IMMUNESCIENCES) 3 June 1992 cited in the application see claims 7,9; example 5	1,2, 10-12, 14,16, 17,19,20
X	US,A,5 139 941 (MUZYCZKA, N. ET AL.) 18 August 1992 see the whole document	1-3
X	WO,A,91 18088 (THE UNITED STATES OF AMERICA, US DEPARTMENT OF COMMERCE) 28 November 1991 cited in the application see page 24, line 35 - page 25, line 24	1,2,16
X	JOURNAL OF CELLULAR BIOCHEMISTRY, vol.SUP, no.18A, 4 January 1994 page 214 CARTER, T. ET AL. 'Adeno-associated virus vectors for in vivo gene transfer' * résumé DZ 001 *	1,2
O,X	& Keystone symposium on gene therapy Copper mountain, USA 15-22 Janvier 1994	1,2
X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA., vol.81, no.20, October 1984, WASHINGTON US pages 6466 - 6470 HERMONAT, P. L. & MUZYCZKA, N. 'Use of adeno-associated virus as a mammalian DNA cloning vector: transduction of neomycin resistance into mammlian tissue culture cells' see page 70, line 1, paragraph IV	1,2,16

1

INTERNATIONAL SEARCH REPORT

Int'l Application No
PCT/FR 95/00054

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/86 C12N15/35 C12N15/27 C12N5/10 C12N7/01

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	VIROLOGY, vol.152, no.1, 15 July 1986 pages 110 - 117 SCHLEHOFER, J.R. ET AL. 'Vaccinia Virus, Herpes Simplex Virus and carcinogens induce DNA amplification in a human cell line and support replication of a helper dependent parvovirus' see page 115, line 5 - line 15; figure 7 ---	1-4,16
X	VIROLOGY, vol.134, no.1, 15 April 1984 pages 64 - 71 GEORG-FRIES, B. ET AL. 'Analysis of proteins, helper dependence and seroepidemiology of a new human parvovirus' see page 68, line 17 - line 22 --- -/--	1-4,16

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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Date of the actual completion of the international search	Date of mailing of the international search report
5 April 1995	02.05.1995

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl, Fax (+ 31-70) 340-3016	Chambonnet, F

INTERNATIONAL SEARCH REPORT

Information on patent family members

I Application No
PCT/FR 95/00054

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
EP-A-0488528	03-06-92	US-A-	5173414	22-12-92
		CA-A-	2054517	01-05-92
		JP-A-	5308975	22-11-93
		US-A-	5354678	11-10-94
US-A-5139941	18-08-92	NONE		
WO-A-9118088	28-11-91	AU-A-	7906691	10-12-91

VIROLOGY 204, 304–311 (1994)

Human Herpesvirus 6 (HHV-6) Is a Helper Virus for Adeno-Associated Virus Type 2 (AAV-2) and the AAV-2 *rep* Gene Homologue in HHV-6 Can Mediate AAV-2 DNA Replication and Regulate Gene Expression

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*Department of Medicine, University of Cambridge, Addenbrooke's Hospital, Cambridge CB2 2QQ, UK; †Deutsches Krebsforschungszentrum, 69120 Heidelberg, Germany; and ‡Max-Planck Institut fur Biochemie, 82152 Martinsried, Germany

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We have previously described the apparent acquisition by human herpesvirus 6 (HHV-6) of the multifunctional *rep* gene of the helper-dependent human parvovirus adeno-associated virus type 2 (AAV-2). We report here that HHV-6 is a full helper virus for AAV-2 replication, suggesting a mechanism for transfer of the *rep* gene between the two viruses by recombination of replicative intermediates. The HHV-6 *rep* gene cloned under control of the human cytomegalovirus immediate early promoter complemented replication of a *rep*-deficient AAV-2 genome. In cotransfection experiments with heterologous promoters linked to the CAT reporter gene, HHV-6 *rep* activated the human immunodeficiency virus (HIV) long terminal repeat (LTR) in fibroblast cell lines but not in T-cells. In contrast, AAV-2 *rep* inhibited HIV LTR activity in both fibroblast and T-cell lines. The effect of HHV-6 and AAV-2 *rep* genes on the HIV LTR was independent of the NF-κB, Sp1, and TATA box elements. These results suggest that HHV-6 Rep is a multifunctional regulatory protein with properties related to, but distinct from, those of AAV-2 Rep.

INTRODUCTION

Human herpesvirus 6 (HHV-6) is a recently isolated member of the herpesvirus family (Salahuddin *et al.*, 1986). Primary infection with HHV-6 usually occurs within the first year of life (Briggs *et al.*, 1988; Okuno *et al.*, 1989) and causes exanthem subitum (Yamanishi *et al.*, 1988). HHV-6 establishes latent infection which can be reactivated following immunosuppression and the virus has been recovered from immunodeficient individuals in many parts of the world (Carrigan *et al.*, 1990; Downing *et al.*, 1987; Lopez *et al.*, 1988; Okuno *et al.*, 1990; Tedder *et al.*, 1987; Ward *et al.*, 1989). HHV-6 has been associated with fatal hepatitis (Asano *et al.*, 1990) and interstitial pneumonitis in bone marrow transplant patients (Carrigan *et al.*, 1991; Cone *et al.*, 1993).

HHV-6 isolates have recently been segregated into two groups on the basis of differences in molecular and biological properties (Ablashi *et al.*, 1993). Variant A viruses are characterized by HHV-6 strain U1102 (Downing *et al.*, 1987) and GS (Salahuddin *et al.*, 1986) and variant B viruses by strain Z29 (Lopez *et al.*, 1988). A restriction endonuclease map of the 160-kb genome of HHV-6 strain U1102 (Downing *et al.*, 1987) has been constructed (Martin *et al.*, 1991b). Nucleotide sequencing studies (Chang and Balachandran, 1991; Efstathiou *et al.*, 1992; Ellinger *et al.*, 1993; Gompels *et al.*, 1992; Josephs *et al.*, 1991; Lawrence *et al.*, 1990; Martin *et al.*, 1991a; Neipel *et al.*, 1991; Teo *et al.*, 1991; Thomson and Honess, 1992) have shown that HHV-6 is most closely related to human cytomegalovirus (HCMV). The unique component of HHV-6 strain U1102 contains an open reading frame (ORF) encoding a 490-amino-acid protein which is homologous to the nonstructural protein Rep 78/68 of the human parvovirus, adeno-associated virus type 2 (AAV-2) (Thomson *et al.*, 1991). A similar ORF has been found in the Z29 strain of HHV-6 (T. R. Dambaugh, personal communication). The AAV-2 *rep* gene is transcribed from two promoters and uses a single alternate splice site to encode overlapping polypeptides identified by their size on acrylamide gels as Rep 78, Rep 68, Rep 52, and Rep 40 (Mendelson *et al.*, 1986; Trempe *et al.*, 1987). Translation of Rep 52 and Rep 40 is initiated at an in-frame methionine which is not present in the HHV-6 sequence. AAV-2 Rep proteins are essential for viral DNA replication (Hermonat *et al.*, 1984; Tratschin *et al.*, 1984) and are required for the regulation of AAV-2 gene expression (Labow *et al.*, 1986; Tratschin *et al.*, 1986; Trempe and Carter, 1988). In addition, AAV-2 Rep downregulates expression from a variety of heterologous promoters (Labow *et al.*, 1987), including the human immunodeficiency virus type 1 (HIV-1) long terminal repeat (LTR) (Antoni *et al.*, 1991; Rittner *et al.*, 1992). Since AAV-2 is a helper-dependent virus which requires either adenoviruses or herpesviruses to achieve productive infection (Buller *et al.*, 1981; Hoggan *et al.*, 1966; McPherson *et al.*, 1985), we hypothesized

[1] To whom reprint requests should be addressed.

0042-6822/94 $6.00

that HHV-6 was a helper virus for AAV-2 and might have acquired the *rep* gene from AAV-2 during co-infection *in vivo* (Thomson *et al.*, 1991). In this paper we show that HHV-6 does indeed provide helper function for AAV-2 DNA replication. We also demonstrate that the HHV-6 *rep* gene homologue can complement replication of a *rep*-deficient AAV-2 genome and regulate gene expression.

MATERIALS AND METHODS

Viruses and cell culture

HeLa cells, Vero cells, and simian virus 40 (SV40) large T-antigen-transformed human skin fibroblast line 1BR were grown at 37° and 5% CO_2 in Dulbecco's modified Eagle's medium with antibiotics (penicillin 10 μg/ml and streptomycin 20 μg/ml) and 10% newborn calf serum. Human CD4+ T-cell lines HSB-2, Molt-3, and J. Jahn were grown in RPMI 1640 medium supplemented with antibiotics and 10% fetal calf serum. AAV-2 was propagated in HeLa cells with adenovirus type 2 as the helper virus, as previously described (Heilbronn *et al.*, 1990; Yalkinoglu *et al.*, 1988). HHV-6 strain variants U1102 and Z29 (Lopez *et al.*, 1988) were propagated on HSB-2 and Molt-3 cells, respectively. Cells were grown at 10^6 cells per milliliter and mixed at a ratio of 5:1 with HHV-6-infected cells from cultures showing a peak cytopathic effect (CPE), usually 7 to 10 days following the previous infection.

Coinfection with HHV-6 and AAV-2

AAV-2 was treated at 56° for 30 min to inactivate helper virus and used to infect HSB-2 or Molt-3 cells at a multiplicity of infection (m.o.i.) of 10 plaque-forming units (PFU). AAV-2-infected cells were then cocultivated with HSB-2 cells which had been previously infected with the U1102 strain of HHV-6 or Molt-3 cells infected with HHV-6 Z29. After full CPE was observed cells were freeze–thawed three times. To demonstrate production of infectious AAV-2, cell-free supernatants were treated at 56° for 30 min to inactivate HHV-6 and then titrated in serial 1:10 dilutions onto HeLa cells using HSV-1 as helper virus as described in Heilbronn *et al.* (1990). Cultures were freeze–thawed and HeLa cell lysates were sucked onto nylon filters. AAV-2 DNA replication was visualized by hybridization with a ^{32}P-labeled AAV-2 probe.

Recombinant plasmids

AAV-2 and HHV-6 *rep* ORFs were both cloned into the pUC19-based expression vector pL15 *tk*, which carries the HCMV immediate early (IE) gene promoter (nucleotides −598 to +52) and a herpes simplex virus thymidine kinase polyadenylation signal (Heilbronn and zur Hausen, 1989). The HHV-6 *rep* gene homologue was cloned as a *KpnI/XbaI* subfragment of *Hin*dIII-C from HHV-6 strain U1102 (Martin *et al.*, 1991b) to yield pCM HHV-6 *rep*. pCM HHV-6 *rep* was digested with *Nco*I (which cleaves a sequence spanning the second in-frame methionine of the *rep* ORF), end-repaired with T4 DNA polymerase, and religated to yield pCM HHV-6 *rep*-. pCM *rep* 78/68, which contains intact ORFs for all four AAV-2 Rep proteins within nucleotides 265 to 2260 and pCM 1906 *rep*, which is C-terminally truncated at the *Kpn*I site at position 1906, and does not encode the second exon of *rep* 68 or *rep* 40, are also based on pL15 *tk* (J. A. Kleinschmidt, M. Mohler, F. W. Weindler, and R. Heilbronn, manuscript in preparation). pR56 expresses the putative HHV-6 IE gene under the control of the HCMV IE gene promoter (Martin *et al.*, 1991a) and was a gift of M. Martin. Cloned *rep*-defective AAV-2 genome pTAV2-3 has been described (Heilbronn *et al.*, 1990). Reporter gene constructs expressed the chloramphenicol acetyl transferase (CAT) gene from the wild type HIV-1 LTR (pLTR.CAT, Sodroski *et al.*, 1985), SV40 early promoter (pSV2.CAT, Gorman *et al.*, 1982), and the HCMV IE promoter (pIE.CAT, a gift of G. Wilkinson described in Kothari *et al.*, 1991). HIV-1 LTR.CAT plasmids containing mutations in the TATA, Sp1, NF-κB, and TAR elements (pDTATA.CAT, pDSp1.CAT, pDNF-κB.CAT and pDTAR.CAT) were gifts from G. Nabel (Nabel *et al.*, 1988).

Transient CAT expression assays

Plasmid DNAs were purified on caesium chloride gradients (Birnboim and Doly, 1979). Monolayers of cell lines HeLa, Vero, and 1BR were transfected essentially as described by Gorman *et al.* (1982). A total of 20 μg DNA was transfected in each experiment, the total being made up when necessary with pUC19. In brief, 2×10^6 cells were plated onto 10-cm-diameter dishes 12 hr prior to transfection, calcium phosphate precipitates applied for 10 hr, and cells harvested 36–48 hours later. T-cell lines were transfected by electroporation as described by Potter *et al.* (1984); 4×10^7 cells in 0.8 ml of RPMI 1640 with no added fetal calf serum were incubated with DNA for 15 min, electroporated at a voltage of 400 mV and a capacitance of 960 μF, and cultured in RPMI 1640 with 10% fetal calf serum for 48 hr before harvest. Cell extracts were quantified for protein concentration (Bio-Rad Protein Assay, Bio-Rad Laboratories) and equal amounts of protein assayed for CAT activity, as described by Gorman *et al.* (1982). Transfections were repeated at least three times and percent conversion of chloramphenicol to monoacetylated forms was quantitated within the linear range of the assay by liquid scintillation counting.

Complementation of AAV-2 replication

Replication of a cloned *rep*-deficient AAV-2 genome (pTAV2-3) by complementation with constructs expressing AAV-2 *rep* (pCM *rep* 78/68) or HHV-6 *rep* (pCM HHV-6 *rep*) was assayed as described in Heilbronn *et al.* (1990). HeLa cells were cotransfected with 4 μg of pTAV2-3 and

36 μg of either pCM *rep* 78/68, pCM HHV-6 *rep*, or empty expression vector (pLT15 *tk*) as a control. Four hours after transfection cells were shocked with DMSO and infected with adenovirus type 2 as helper virus at an m.o.i. of 2. Cells were harvested 72 hr postinfection. Genomic DNA was extracted, digested with *Xba*I and *Dpn*I, and transferred onto nylon filters. Filters were then hybridized with ^{32}P-labeled AAV-2.

RESULTS

HHV-6 is a helper virus for AAV-2 DNA replication

In order to investigate the possibility that HHV-6 is a helper virus for AAV-2 replication, the human T-cell line HSB-2 was co-infected with AAV-2 and HHV-6 strain variant U1102. At the time of peak CPE, cells were freeze–thawed and then treated at 56° to inactivate HHV-6. In order to detect the presence of infectious AAV-2, cell-free supernatants were titrated onto indicator HeLa cells using HSV-1 as helper virus. Transfer of infectious AAV-2 was monitored by hybridization of indicator cell DNA with a ^{32}P-labeled AAV-2 probe. As illustrated in Fig. 1, co-infection of HSB-2 cells with HHV-6 strain U1102 clearly led to productive infection with AAV-2, as assessed by the transfer of infectious AAV-2 to the indicator cell line. In contrast, infection of HSB-2 cells with AAV-2 alone did not lead to the transfer of infectious virus. Similar results were obtained using HHV-6 strain variant Z29 to provide help for AAV-2 replication in the Molt-3 cell line (Fig. 1).

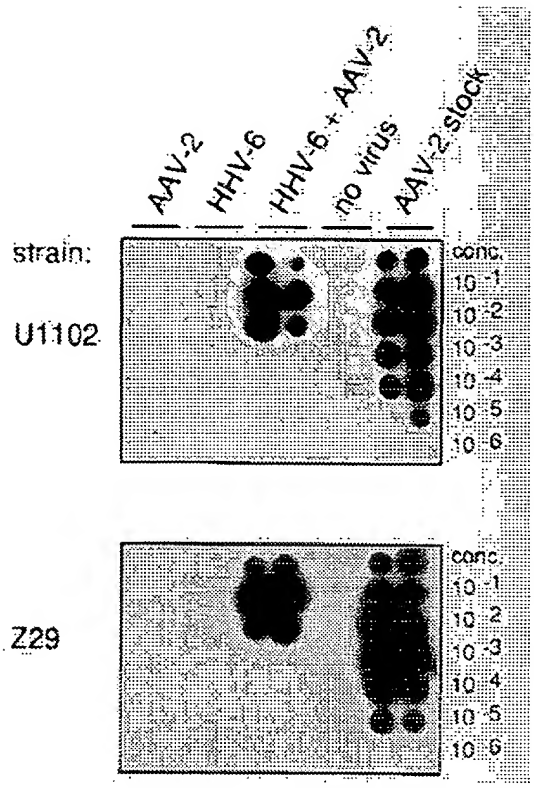

FIG. 1. HHV-6 is a full helper virus for the production of infectious AAV-2. HSB-2 cells were infected with AAV-2, HHV-6 strain variant U1102, or both, as described under Materials and Methods. The lower figure shows the results of experiments in which Molt-3 cells were infected in a similar manner using HHV-6 strain variant Z29. Cell-free supernatants harvested from HSB-2 or Molt-3 cells were titrated in serial 1:10 dilutions onto Hela cells using HSV-1 as helper virus. Transfer of infectious AAV-2 was visualized by hybridization of HeLa cell DNA with a ^{32}P-labeled AAV-2 probe (concentration to 10^{-6} indicated the dilution of infectious AAV-2 stock of known titer titrated in parallel as a positive control).

The HHV-6 *rep* gene homologue can complement r plication of a *rep*-deficient AAV-2 genome

In order to assess the potential function of the HHV-6 *rep* gene homologue, the capacity of pCM HHV-6 *rep* to complement replication of a cloned *rep*-defective AAV-2 genome (pTAV2-3) was studied. HeLa cells were cotransfected with pTAV2-3 and constructs expressing AAV-2 *rep* (pCM *rep* 78/68), HHV-6 *rep* (pCM HHV-6 *rep*), or equimolar amounts of the empty expression vector (pL15 *tk*). Cells were infected with adenovirus type 2 as helper virus; 72 hr post-transfection total genomic DNA was extracted and double digested with *Xba*I and *Dpn*I. AAV-2 DNA replication was monitored on Southern blots probed with ^{32}P-labeled AAV-2 DNA (Fig. 2). pCM *rep* 78/68, which expressed full-length AAV-2 Rep proteins (data not shown), mediated accumulation of the typical replicative intermediates RF1 (4.7 kb, double-stranded monomer) and RF2 (9.4 kb, double-stranded dimer). Cotransfection of pTAV2-3 with pCM HHV-6 *rep* clearly resulted in the accumulation of RF1 and RF2, although at a somewhat lower efficiency than the wild type AAV-2 Rep proteins. The levels of mRNA expressed by pCM-HHV-6 *rep* and pCM *rep* 78/68 following parallel transfections were comparable (data not shown). Absolutely no AAV-specific signal is detected upon cotransfection of pTAV2-3 with the empty expression vector (pL15 *tk*).

The HHV-6 *rep* gene homologue regulates the HIV-1 LTR

The AAV-2 *rep* gene has been shown to downregulate HIV LTR-driven gene expression (Antoni *et al.*, 1991; Rittner *et al.*, 1992). Since HHV-6 and HIV both infect CD4+ lymphocytes *in vivo*, we assessed whether the HHV-6 *rep* gene was also capable of modulating HIV gene expression. Vero cells were cotransfected with CAT reporter constructs driven by selected heterologous promoters and a 5-fold molar excess of empty expression vector (pL15 *tk*) or expression vectors pCM HHV-6 *rep*, pCM HHV-6 *rep*-, pCM *rep* 78/68, or pCM *rep* 1906. pCM *rep* 1906 expresses a C-terminally truncated version of *rep* 78/68 corresponding closely to the region homologous to HHV-6. The results of these experiments are

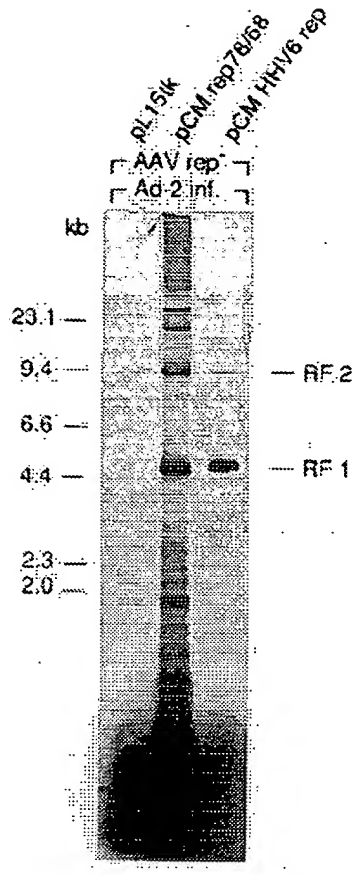

FIG. 2. The HHV-6 *rep* gene mediates replication of a *rep*-defective AAV-2 mutant (pTAV2-3). Hela cells were cotransfected with 4 μg pTAV2-3 and 36 μg of empty expression vector pL15 *tk* or effector plasmids pCM *rep* 78/68 and pCM HHV-6 *rep*. Cells were superinfected with adenovirus type 2 as helper virus. Genomic DNA was digested with *Dpn*I and *Xba*I (which does not cut within the AAV-2 genome) and Southern blots were probed with ^{32}P-labeled AAV-2 DNA. *Dpn*I digests transfected DNA which has been methylated during prokaryotic replication (visible as low-molecular-weight bands in the lower part of the blot). Following replication in eukaryotic cells transfected DNA is not methylated and becomes *Dpn*I resistant. The typical replicative intermediates of AAV-2 are indicated — RF1 represents monomeric double-stranded DNA of 4.7 kb in length and RF2 double-stranded dimers of 9.4 kb in length.

shown in Figs. 3a and 3b. The empty expression vector (pL15 *tk*) was used as a control in all experiments. In all experiments, pCM *rep* 78/68 and pCM *rep* 1906 completely suppressed HIV-1 LTR-driven CAT expression in Vero cells. In contrast, transfection of pLTR.CAT with pCM HHV-6 *rep* increased CAT gene expression by a factor of between 5- and 10-fold compared to equimolar amounts of the empty expression vector (pL15 *tk*). Induction of CAT expression by pCM HHV-6 *rep*-, containing a frame-shifting mutation in the *rep* ORF, did not differ significantly from controls (Figs. 3a and 3b). These experiments were repeated in 1BR cells with similar results (data not shown). Activation of the HIV LTR by pCM HHV-6 *rep* in Vero and 1BR cells was similar to that induced by the putative HHV-6 IE gene expressing plasmid pR56 (Fig. 3a). As controls, the effects of cotransfection of Rep-expressing plasmids on CAT gene expression from the SV40 early promoter (pSV2.CAT) and HCMV IE promoter (pIE.CAT) in Vero cells are also shown in Fig. 3b. At 5-fold molar excess, both pCM 78/68 *rep* and pCM *rep* 1906 downregulated expression from pSV2.CAT, but not from pIE.CAT, as previously documented (Beaton *et al.*, 1989; Heilbronn *et al.*, 1990). Transfection of pCM HHV-6 *rep* had no effect in either SV40- or HCMV-driven gene expression in these experiments. To test whether HHV-6 *rep* could enhance expression from the HIV-LTR in T-cells, pCM *rep* 78/68, pCM *rep* 1906, and pCM HHV-6 *rep* were transfected together with pLTR.CAT into J. Jahn cells. A total of 20 μg of pLTR.CAT was needed to provide measurable basal CAT activity in these cells, and as quantitative introduction of DNA into J. Jahn cells was limited to 40 μg (data not shown), the ratio of effector to reporter plasmid DNA was limited to 1:1. Under these conditions, both AAV-2 *rep* expression constructs downregulated CAT expression from the HIV LTR, whereas pCM HHV-6 *rep* had no significant effect on CAT activity (Fig. 3c). We assume that higher molar ratios are required for activation by HHV-6 *rep*. In control experiments in J. Jahn cells, pCM 78/68 *rep* and pCM 1906 *rep* did not inhibit CAT gene expression from the HCMV IE promoter (Fig. 3c). In order to identify *cis* elements required to mediate these effects, HIV.LTR deletion mutants linked to CAT were transfected into Vero cells. Mutants with deletions in the TATA box (pDTATA.CAT), Sp1 (pDSp1.CAT), NF-κB (pDNF-κB), and TAR (pDTAR.CAT) elements mediated downregulation by pCM 78/68 and pCM *rep* 1906 and induction by pCM HHV-6-*rep* with an efficiency which did not differ significantly from that of the wild type HIV LTR (Fig. 4).

DISCUSSION

We have shown that two isolates of HHV-6, strains U1102 and Z29, provide full helper function for AAV-2 replication. These isolates are representative of each of the groups of HHV-6 (strain U1102 is characteristic of variant A viruses and strain Z29 of variant B viruses) (Ablashi *et al.*, 1993). HHV-6 is tropic for CD4+ T-lymphocytes *in vitro* (Lusso *et al.*, 1988) and *in vivo* (Takahashi *et al.*, 1989). Although the cellular tropism of AAV-2 *in vivo* has not been established, the virus has been shown to replicate in both CD4+ T-cell lines (Mendelson *et al.*, 1992) and peripheral blood lymphocytes (PBL) (Grossman *et al.*, 1992) *in vitro*. DNA from HHV-6 (Gopal *et al.*, 1990) and AAV-2 (Grossman *et al.*, 1992) has been found in PBL of healthy adults by the polymerase chain reaction. HHV-6 is therefore a good candidate for a helper virus active *in vivo*, providing a means by which HHV-6 could have acquired the *rep* gene from AAV-2 by recombination between replicative intermediates.

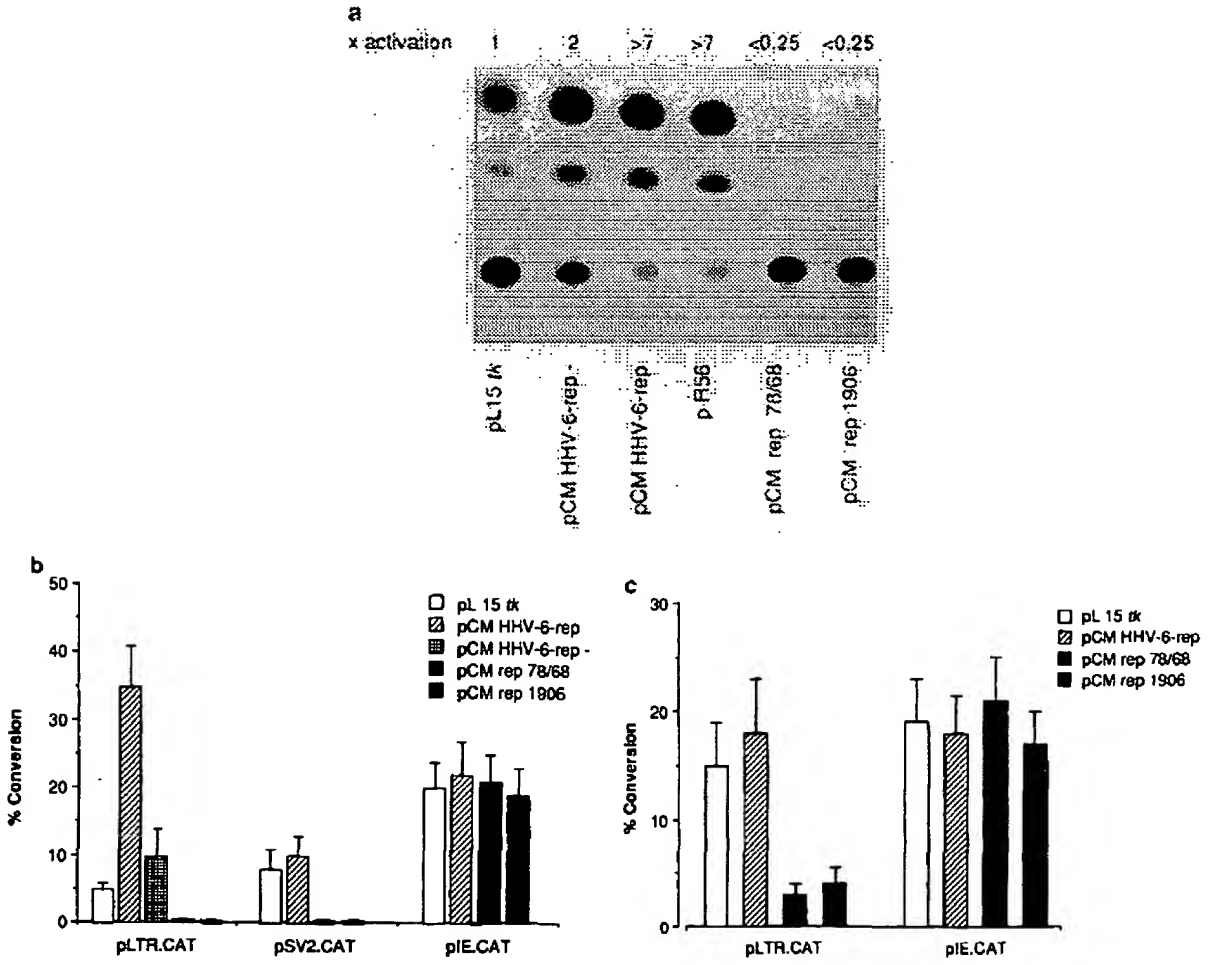

FIG. 3. (a) HHV-6 *rep* transactivates the HIV-1 LTR in Vero cells. Empty expression vector pL15 *tk* or expression plasmids pCM HHV-6 *rep*, pCM HHV-6 *rep*-, pR56, pCM *rep* 78/68, and pCM *rep* 1906 were transfected at fivefold molar excess with pLTR.CAT (1 μg) in Vero cells. Total DNA transfected was 20 μg, made up with pUC19. CAT activity is calculated as the percent conversion of chloramphenicol to monoacetylated forms as assessed by liquid scintillation counting within the linear range of the assay; x activation is CAT activity in each track divided by CAT activity in the control track (transfection with empty expression vector pL15 *tk*). (b) The mean of three experiments in which pCM HHV-6 *rep*, pCM HHV-6 *rep*-, pCM *rep* 78/68, and pCM *rep* 1906 were cotransfected with selected reporter gene constructs. 1 μg of pLTR.CAT, 4 μg of pSV2.CAT, and 1 μg of pIE.CAT were each transfected with a fivefold molar excess of effector plasmids. The empty expression vector (pL15 *tk*) was used as a control in all experiments. CAT activity was calculated within the linear range of the assay and standard errors are shown. (c) The effect of HHV-6 and AAV-2 *rep* on expression of the CAT gene from heterologous promoters in T-cell line J. Jahn. 20 μg pLTR.CAT and 10 μg pIE.CAT were introduced by electroporation with equimolar amounts of empty expression vector (pL15 *tk*) or effector plasmid. Each experiment was performed at least three times and the standard errors are shown.

The function of the *rep* gene homologue in the life cycle of HHV-6 is currently unknown. The HHV-6 *rep* gene is more closely related to the nonstructural AAV-2 Rep 78/68 protein than are the homologous proteins encoded by other members of the parvovirus family (Thomson *et al.*, 1991). Results presented in this paper show that the HHV-6 gene can mediate the accumulation of AAV-2 replicative forms and therefore possesses at least some of the properties of the AAV-2 Rep protein. The nonstructural protein of the autonomous parvovirus B19, which is less closely r lated to AAV-2 *rep* than is the HHV-6 gene, has also been shown to replicate a recombinant genome with AAV-2 termini (Srivastava *et al.*, 1989). The AAV-2 Rep 78 and Rep 68 proteins bind to AAV-2 terminal hairpin structures and have a site-specific, ATP-dependent endonuclease and helicase activity (Im and Muzyczka, 1990, 1992). Parvovirus Rep proteins each contain a domain homologous to a conserved region of large T-antigen of SV40 and polyomavirus and the E1 protein of papillomaviruses (Astell *et al.*, 1987). This domain, which is well conserved in the HHV-6 *rep* homologue (Thomson *et al.*, 1991), includes an NTP binding site and is characteristic of DNA and RNA helicases encoded by a number of unrelated viruses (Gorbalenya

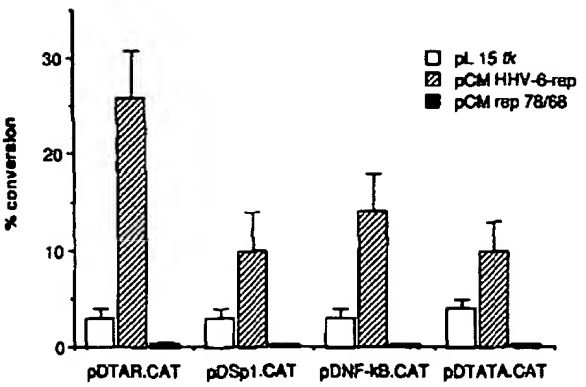

FIG. 4. The results of transfection of a series of mutant HIV LTR.CAT constructs with control plasmid (pLT15 *tk*) and effector plasmids pCM HHV-6 *rep* and pCM *rep* 78/68 in Vero cells. 1 μg pDTAR.CAT or 4 μg pDSp1.CAT, pDNF-κB.CAT, and pDTATA.CAT (gifts of G. Nabel) were cotransfected with a fivefold molar excess of empty expression vector pL15 *tk* or expression plasmids. CAT activity is expressed as percent conversion of chloramphenicol to monoacetylated forms as assessed by liquid scintillation counting within the linear range of the assay. Experiments were performed at least three times and the standard errors are illustrated.

et al., 1990). Our results, together with these structural features, suggest that the HHV-6 *rep* gene homologue can function as a helicase *in vivo*.

The Rep 78/68 protein positively regulates the AAV-2 p_{40} promoter in the presence of helper virus (Tratschin *et al.*, 1986), but negatively autoregulates (Beaton *et al.*, 1989) and suppresses expression from a number of heterologous promoters (Antoni *et al.*, 1991; Labow *et al.*, 1986; Rittner *et al.*, 1992; Tratschin *et al.*, 1986). These effects can be mediated at the level of both transcription and translation (Trempe and Carter, 1988). We have shown that suppression of the HIV LTR by AAV-2 Rep proteins occurred in CD4+ T-cells in addition to the adherent cells lines previously reported (Antoni *et al.*, 1991; Rittner *et al.*, 1992). Furthermore, the function of the C-terminally truncated protein expressed by pCM *rep* 1906 could not be distinguished from wild type, indicating that C-terminal sequences which distinguish Rep 78 from Rep 68 (J. A. Kleinschmidt, M. Mohler, F. W. Weindler, and R. Heilbronn, manuscript in preparation) are not required for downregulation of the heterologous promoters tested. In contrast, the HHV-6 gene positively regulated the HIV LTR with an efficiency comparable to that of the HHV-6 major IE gene identified by Martin *et al.* (1991a). These results do not distinguish transcriptional from translational effects and the mechanisms of gene regulation by the Rep proteins remains to be determined. HHV-6 has been shown to upregulate expression from the HIV-1 LTR (Horvat *et al.*, 1989; Ensoli *et al.*, 1989) and co-infection of CD4+ cells with HHV-6 been found to both enhance (Lusso *et al.*, 1989) and suppress (Carrigan *et al.*, 1990) HIV replication. Activation by infectious HHV-6 and by some genomic fragments is NF-κB dependent (Ensoli *et al.*, 1989; Geng *et al.*, 1992; Horvat *et al.*, 1991). Regulation of the HIV LTR by AAV-2 *rep* and the HHV-6 homologue, in common with the HHV-6 major IE gene (Martin *et al.*, 1991a), appears to be independent of the Sp1, NF-κB, and TATA box elements. A recent study, published after this work was submitted, has confirmed our observation that downregulation of the HIV LTR by the AAV-2 *rep* gene does not require Sp1 or NF-κB elements (Oelze *et al.*, 1994). It will be interesting to see whether HHV-6 *rep* is a regulator of HHV-6 genes *in vivo*.

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High-titer recombinant adeno-associated virus production utilizing a recombinant herpes simplex virus type I vector expressing AAV-2 Rep and Cap

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Recombinant adeno-associated virus type 2 (rAAV) vectors have recently been used to achieve long-term, high level transduction in vivo. Further development of rAAV vectors for clinical use requires significant technological improvements in large-scale vector production. In order to facilitate the production of rAAV vectors, a recombinant herpes simplex virus type I vector (rHSV-1) which does not produce ICP27, has been engineered to express the AAV-2 rep and cap genes. The optimal dose of this vector, d27.1-rc, for AAV production has been determined and results in a yield of 380 expression units (EU) of AAV-GFP produced from 293 cells following transfection with AAV-GFP plasmid DNA. In addition, d27.1-rc was also efficient at producing rAAV from cell lines that have an integrated AAV-GFP provirus. Up to 480 EU/cell of AAV-GFP could be produced from the cell line GFP-92, a proviral, 293 derived cell line. Effective amplification of rAAV vectors introduced into 293 cells by infection was also demonstrated. Passage of rAAV with d27.1-rc results in up to 200-fold amplification of AAV-GFP with each passage after coinfection of the vectors. Efficient, large-scale production (> 10^9 cells) of AAV-GFP from a proviral cell line was also achieved and these stocks were free of replication-competent AAV. The described rHSV-1 vector provides a novel, simple and flexible way to introduce the AAV-2 rep and cap genes and helper virus functions required to produce high-titer rAAV preparations from any rAAV proviral construct. The efficiency and potential for scalable delivery of d27.1-rc to producer cell cultures should facilitate the production of sufficient quantities of rAAV vectors for clinical application.

Keywords: *adeno-associated virus; herpes simplex virus; rAAV; gene therapy; vector production*

Introduction

Recombinant adeno-associated virus type 2 vectors (rAAV) have been extremely successful vectors for *in vivo* gene transfer. These vectors have produced long-term, high-level gene expression of therapeutic proteins in immunocompetent animal models. For example, sustained production of erythropoietin from skeletal muscle after rAAV transduction has been achieved in mice.[1] Therapeutic levels of factor IX have been produced after rAAV gene transfer to the liver and skeletal muscle.[2–5] Levels of therapeutic protein production have reached up to 800 μg/ml in mice treated intramuscularly with AAV vectors expressing alpha-1 antitrypsin.[6] Recombinant AAV vectors have been used effectively in the central nervous system.[7–9] In addition, rAAV has been used in human clinical trials to transfer the CFTR gene.[10]

Production of sufficient quantities of high-titer rAAV needed for effectiveness *in vivo* has been difficult to achieve, however. The process requires the efficient cellular delivery of the proviral construct to be packaged as rAAV, the AAV-2 *rep* and *cap* genes, as well as specific helper virus functions.[11] The proviral construct to be packaged contains the cDNA expression cassette flanked by AAV-2 inverted terminal repeats (ITRs). The ITRs are the *cis* acting viral DNA sequences required to direct replication and packaging of the rAAV vector.[12,13] AAV-2 *rep* and *cap* genes encode the four Rep proteins (Rep 78, 68, 52 and 40) involved in viral DNA replication, resolution of replicative intermediates and generation of single-strand genomes and the three structural genes (VP1, VP2 and VP3) that make up the viral capsid.[14–16] Usually, the proviral rAAV and the *rep* and *cap* genes are introduced into cells by plasmid transfection. Replication and packaging of rAAV then occurs after expression of specific genes from a helper virus such as adenovirus (Ad).[14,17–20] Traditionally, Ad infection is used to provide helper virus functions.[11] In the case of Ad, the specific helper functions have been identified as the E1a, E1b, E2a, E4orf6 and Va RNA genes. These Ad genes encode proteins or RNA transcripts which are transcriptional regulators and are involved in DNA replication or modify the cellular environment in order to permit efficient viral production.[14,17–20]

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Recent improvements in rAAV packaging technology have made production of high-titer rAAV more feasible. One significant advancement has been the development of an Ad-free method for rAAV production.[20,21] This method is based on transfection of a plasmid encoding the Ad helper functions required for the production of rAAV. Other improvements have included the generation of *rep* inducible cell lines, translational control of Rep production and increasing Cap expression by driving *cap* transcription with a strong heterologous promoter.[22–24] These improved methods still possess limitations, however. The *rep* inducible cell lines do not produce rAAV more efficiently than traditional methods. Translational and transcriptional control of Rep and Cap production do not increase the efficiency of rAAV production more than 10-fold.[23,24] The Ad free method requires successful transfection on a large scale that is not easily achieved.

While Ad is an efficient helper virus for rAAV production, little consideration has been given to other helper viruses for AAV-2 replication and packaging. Herpes simplex virus type 1 (HSV-1) is also a fully competent helper virus of AAV-2.[25–28] The minimal set of HSV-1 genes required for AAV-2 replication and packaging has been identified as the early genes UL5, UL8, UL52 and UL29.[28] These genes encode components of the HSV-1 core replication machinery – the helicase, primase and primase accessory proteins and the single-stranded DNA binding protein (reviewed in Refs 29 and 30).

We have investigated the use of a recombinant HSV-1 (rHSV-1) vector to facilitate production of rAAV. A rHSV-1 has been engineered to express the AAV-2 *rep* and *cap* genes (*d27.1-rc*). This rHSV-1 vector, *d27.1-rc*, does not produce ICP27, a protein required for HSV-1 replication. Although *d27.1-rc* is replication defective, it does express the HSV-1 early genes required for rAAV replication and packaging.[28,31]

The vector *d27.1-rc* has been found to be as efficient at producing rAAV as Ad-free methods and obviates the need for large-scale transfection protocols. In addition, the rHSV-1 vector is 100 times more efficient at producing rAAV than previously described amplicon system based on the HSV-1 helper functions.[32] The rHSV vector, *d27.1-rc*, is a novel, flexible and simple way to introduce the AAV-2 *rep* and *cap* genes and helper virus functions required to produce high-titer rAAV preparations. The potential for scaleable rAAV growth using *d27.1-rc* should facilitate production of sufficient quantities of rAAV vectors required for clinical applications.

Results

Construction and characterization of d27.1-rc

The rHSV-1, *d27.1-rc* was constructed by homologous recombination of the AAV-2 *rep* and *cap* genes into the *tk* locus of the rHSV-1 virus *d27.1* (Figure 1). In this recombinant virus, the AAV-2 *rep* and *cap* genes are under control of their native promoters – the p5, p19 and p40 promoters. The p5, p19 and p40 promoters drive expression of the AAV-2 proteins Rep 78 and 68, Rep 52 and 40 and the capsid structural proteins VP1, VP2 and VP3, respectively.[33–37] Homologous recombination into the *tk* gene was confirmed by Southern blot analysis of restriction digests of *d27.1-rc* infected cell DNA (data not shown). In addition, *d27.1-rc* plaque formation on V27 cells, a complementing cell line, was not affected by 5-bromo-deoxycytidine. This indicates that the *tk* gene, appropriately, did not produce functional thymidine kinase (data not shown).

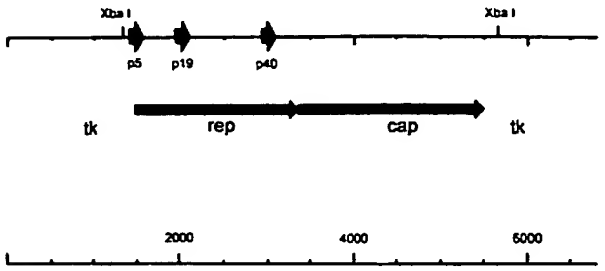

Figure 1 Schematic of the integration vector pHSV-106-rc. The plasmid pHSV-106 contains the BamHI fragment encoding the tk gene of HSV-1. The AAV-2 rep and cap genes, under control of their native promoters, were cloned into the KpnI site of tk gene to generate pHSV-106-rc. Restriction digest of pHSV-106-rc with SphI was used to generate the linear fragment. This fragment was cotransfected with d27.1-lacZ infected cell DNA into V27 cells to generate d27.1-rc by homologous recombination.

Production of AAV-2 Rep by d27.1-rc

In order for *d27.1-rc* to compliment rAAV replication, the AAV-2 Rep proteins must be efficiently expressed and localized to the nucleus of the cell after *d27.1-rc* infection. To determine the level of expression of the AAV-2 Rep proteins from *d27.1-rc*, Western analysis was utilized. The expression of the AAV-2 Rep proteins from *d27.1-rc* after infection of three different cell lines (293, Vero and V27 cells) at different multiplicities of infection (MOI) was analyzed (Figure 2).

The vector *d27.1-rc* expressed different levels of each of the AAV-2 Rep proteins in the different cell lines (Figure 2). In 293 cells, high level expression of all four Rep proteins occurred after infection with *d27.1-rc*. Expression of the Rep proteins was also observed in Vero cells after *d27.1-rc* infection. In contrast, only a small amount of Rep was produced in V27 cells after *d27.1-*

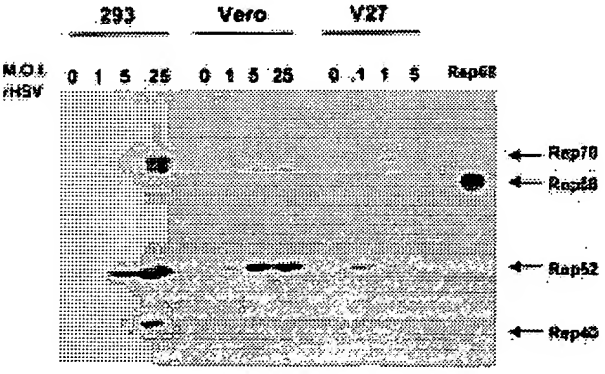

Figure 2 Western analysis was performed to determine the expression of the AAV-2 Rep proteins from d27.1-rc. The expression of the AAV-2 Rep proteins from d27.1-rc after infection of three different cell types (293, Vero and V27 cell lines) at different MOIs was determined. The highest level of Rep expression was observed in 293 cells. Rep expression was also detected in Vero cells. Minimal Rep expression was observed in V27 cells, especially at higher MOIs.

rc infection, especially at higher MOIs. The level of Rep expression after *d27.1-rc* infection of 293 and Vero cells was observed to be dependent on the MOI. The higher level expression of Rep in 293 cells after *d27.1-rc* infection may be due to up-regulation of the p5 promoter by Ad E1a present in 293 cells. The low level of Rep expressed in V27 cells after *d27.1-rc* infection in part results from lytic replication of *d27.1-rc* after infection of this cell line.

The Rep produced by d27.1-rc localizes to the nucleus

The cellular distribution of the AAV-2 Rep proteins was determined in an immunofluorescence assay (IFA) which utilized a monoclonal antibody that recognizes the four Rep proteins. The Rep proteins, expressed after infection of 293 cells by *d27.1-rc*, localized to discrete nuclear punctate bodies (Figure 3a). The distribution of Rep proteins to the nucleus of 293 cells infected with *d27.1-rc* is a prerequisite for rAAV replication.

Replication center formation by d27.1-rc

The observation has been made that the *rep* gene products are capable of inhibiting viral and cellular DNA replication.[38–40] In particular, *rep* gene products have been shown to be potent inhibitors of Ad DNA replication and prevent the maturation of Ad DNA replication centers.[41] This inhibitory effect of Rep proteins is presumably responsible for the inability to generate a recombinant Ad that expresses the AAV-2 *rep* gene. If *rep* gene products similarly inhibited HSV-1 viral DNA replication, the recombinant virus, *d27.1-rc*, would not be able to propagate. Replication of *d27.1-rc* was not affected by the presence of the *rep* gene, however. The kinetics of plaque formation on V27 cells, the complementing cell line, and the amount of virus produced per cell was identical to the parent virus, *d27.1* (data not shown).

In addition, the development of HSV-1 DNA replication centers after *d27.1-rc* infection of V27 cells was not affected by the presence of the *rep* gene. HSV-1 replication centers develop in the nuclei of infected cells in a time-dependent manner.[42] Viral and cellular proteins required for viral DNA replication (such as the HSV-1 core replication proteins which include ICP8, the single-stranded DNA binding protein) and replicating viral DNA localize to these centers.[42–45] Mature HSV-1 replication centers were observed in the nuclei of V27 cells 12 h after *d27.1-rc* infection, as indicated by the distribution of ICP8 (Figure 4a). This distribution of ICP8 is characteristic of fully developed HSV-1 replication centers[45] and did not differ from replication centers formed in V27 cells by the parent virus, *d27.1* (data not shown). In addition, minimal AAV-2 Rep expression was observed in V27 cells after *d27.1-rc* infection (Figure 4b).

The vector d27.1-rc is efficient at producing infectious rAAV from different rAAV proviral templates

To determine the flexibility and efficiency of rAAV production using *d27.1-rc*, we tested the production of rAAV from proviral plasmid transfected into cells, from a proviral cell line and by amplifying rAAV by coinfection. The vector *d27.1-rc* was observed to effectively rescue rAAV from pTR-UF5-transfected 293 cells. The plasmid pTR-UF5 contains a proviral rAAV genome that encodes the green fluorescent protein (GFP).[46] Transfection of 293 cells with pTR-UF5 followed by super-infection with *d27.1-rc* resulted in rescue of infectious AAV-GFP (Figure 5a and b). The amount of AAV-GFP produced was a function of the MOI of *d27.1-rc*. An increase in the yield of AAV-GFP was observed up to an MOI of 10. At this MOI, the yield of AAV-GFP was 381 expresion units (EU) per cell. This level of production compares favorably with recently developed rAAV production protocols based upon Ad-free transfection procedures.[20,21] Infection of pTR-UF5-transfected 293 cells with a control virus, *d27.1-lacz*, at an MOI of 10 did not produce AAV-GFP (data not shown).

The vector *d27.1-rc* was also capable of efficient AAV-GFP production from the cell line GFP-92 (Figure 6). In the cell line GFP-92, a proviral rAAV genome that encodes GFP is integrated into the chromosomal DNA. As in the transfection experiment, the amount of AAV-GFP produced was observed to be a function of the MOI of *d27.1-rc*. At the most efficient MOI for AAV-GFP replication and packaging, 480 EU/cell could be produced using the vector *d27.1-rc*. Infection of this cell line with the control virus *d27.1-lacz* at an MOI of 10 did not produce AAV-GFP (data not shown).

Amplification of rAAV via co-infection with rHSV

Interestingly, *d27.1-rc* can also be used to amplify rAAV genomes introduced into cells by infection of rAAV

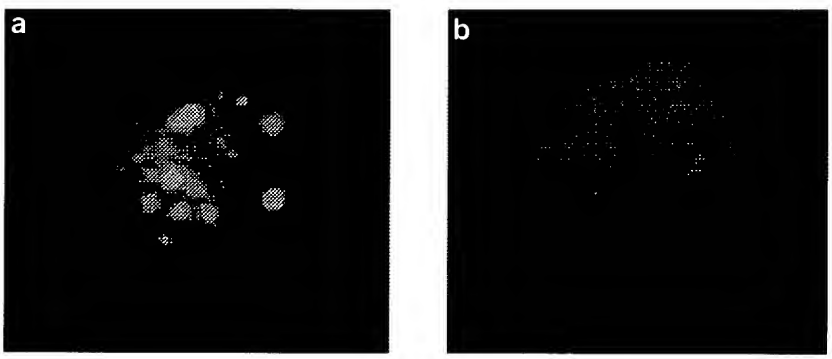

Figure 3 (a) Immunofluorescence assay detecting the distribution of the AAV-2 Rep proteins, 10 h after infection of 293 cells with d27.1-rc. The 293 cells were processed for IFA and the cells were incubated with a monoclonal antibody that detects all four Rep proteins (78, 68, 52 and 40). The cells were then incubated with a FITC-conjugated, donkey anti-mouse secondary antibody. Magnification ×630. (b) DAPI counterstain of the nucleus in (a). Magnification ×630.

Figure 4 Immunofluorescence assay showing the development of mature HSV-1 viral DNA replication centers and minimal Rep expression in V27 cells after infection with d27.1-rc. Twelve hours after infection (MOI of 1), V27 cells were processed for IFA and incubated with a rabbit, anti-ICP8 antibody and a monoclonal, anti-Rep antibody. The cells were then incubated with a rhodamine-conjugated, donkey anti-rabbit secondary antibody and a FITC-conjugated, donkey anti-mouse secondary antibody. (a) Distribution of ICP8 in V27 cells infected with d27.1-rc. The observed nuclear distribution of ICP8 is characteristic of mature HSV-1 replication centers. Magnification ×630. (b) Rep expression is not detected in V27 cells infected with d27.1-rc. Magnification ×630. (c) DAPI counterstain of the nuclei in (a) and (b). Magnification ×630.

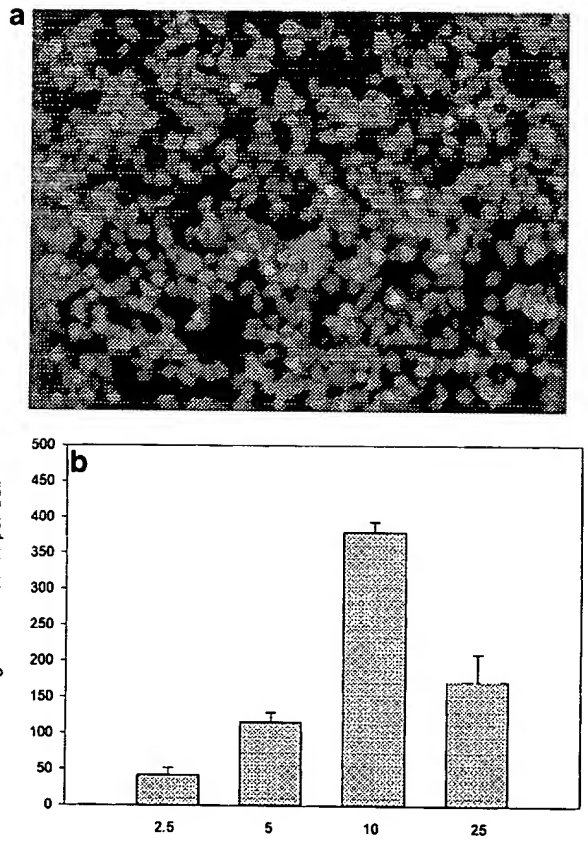

Figure 5 (a) Purified AAV-GFP produced by d27.1-rc is infectious. C12 cells were infected with the AAV-GFP (MOI 5 EU) produced by d27.1-rc. The cells were then coinfected with Ad (MOI 20). Fluorescent microscopy was used to detect GFP expression 24 h after infection. Magnification ×100. (b) The vector d27.1-rc can efficiently produce rAAV from transfected 293 cells. 293 cells were transfected with AAV-GFP proviral plasmid. (Approximately 3× 10^7 cells were present in each experimental group.) Twenty-four hours after transfection, the cells were superinfected with different MOIs of d27.1-rc. Thirty-six hours after infection, a cell lysate was made from the infected cells by three rounds of freeze–thaw. The cell lysate was heat inactivated at 55°C for 1 h and then titered in duplicate on C12 cells that were co-infected with Ad (MOI 20). Forty-eight hours after infection the C12 cells were analyzed for GFP expression using fluorescent microscopy and a titer was determined (in EU). The amount of AAV-GFP produced per transfected cell was then calculated. The data represent triplicate experiments.

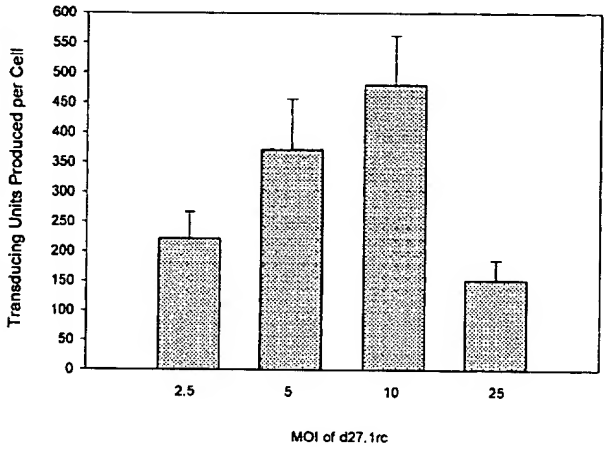

Figure 6 The vector d27.1-rc can produce rAAV from an AAV-GFP proviral cell line. The cell line GFP-92 is a 293-derived cell line that has a single copy of AAV-GFP integrated into its genome. The vector d27.1-rc was used to produce AAV-GFP from this cell line. 1.5× 10^7 GFP-92 cells were infected with d27.1-rc at different MOIs. Forty-eight hours after infection a cell lysate was made from the infected cells by three rounds of freeze–thaw. The cell lysate was heat inactivated at 55°C for 1 h and then titered in duplicate on C12 cells that were co-infected with Ad (MOI 20). Forty-eight hours after infection the C12 cells were analyzed for GFP expression using fluorescent microscopy and a titer was determined (EU). The amount of AAV-GFP produced per transfected cell was then calculated. The data represent triplicate experiments.

(Table 1). When rAAV and rHSV are co-infected in 293 cells, amplification of rAAV genomes is observed. Infection with *d27.1-rc* (MOI of 10) along with rAAV (MOI = 0.1) leads to a 200-fold amplification of input AAV-GFP. The total amplification of rAAV was greater than 10^6-fold after three cycles of passage. While not as efficient as the production of AAV-GFP from transfected plasmid or a proviral cell line, co-infection of rAAV vectors with *d27.1-rc* will permit serial amplification of rAAV via scaleable infection.

The efficiency of rAAV production by d27.1-rc is maintained when the scale of production is increased

To determine if *d27.1-rc* can be utilized to produce rAAV on a larger scale, 10^9 GFP-92 cells were infected with *d27.1-rc* (Table 2). The yield of AAV-GFP, 380 EU/cell and 338 EU/cell in duplicate experiments, indicates that *d27.1-rc* is still able to efficiently produce rAAV after the

Table 1 Serial passage of rAAV with *d27.1-rc* results in vector amplification

Passage No.	Input vector	Output vector	Fold amplification	Total amplification
1	5.0×10^3	1.0×10^6	200	200
2	1.0×10^4	1.75×10^6	175	3.5×10^4
3	1.75×10^6	2.97×10^7	170	5.95×10^6

Recombinant adeno-associated virus can be amplified after co-infection with *d27.1-rc*. 293 Cells were infected with different MOIs of AAV-GFP as indicated. Twelve hours after infection, the cells were superinfected with *d27.1-rc* at a MOI of 10. Forty-eight hours after infection a cell lysate was made from the infected cells by three rounds of freeze–thaw. The cell lysate was heat inactivated at 55°C for 1 h and then titered in duplicate on C12 cells that were co-infected with adenovirus (MOI 20). Forty-eight hours after infection the C12 cells were analyzed for GFP expression using fluorescent microscopy and a titer was determined (EU). The data represent duplicate experiments.

Table 2 Efficient large-scale production of rAAV is observed using *d27.1-rc*

Experiment No.	No. of GFP-92 cells	Amount of virus produced in cell lysate (EU)	EU produced per cell
1	1.0×10^9	3.8×10^{11}	380
2	1.1×10^9	3.7×10^{11}	338

scale of infection is increased. Maintaining efficient rAAV production as the scale of *d27.1-rc* infection is increased is required if *d27.1-rc* is a viable helper for large-scale production of rAAV.

Discussion

Recombinant adeno-associated virus-mediated gene transfer has been uniquely successful in achieving long-term, high-level gene expression *in vivo*. Many potential applications for the use of rAAV in genetic disease will require a substantial vector dose to achieve a therapeutic effect. One significant problem associated with rAAV vectors, has been the difficulty in generating sufficient quantities of high-titer vector required for *in vivo* applications. This difficulty has led to improvements in numerous aspects of rAAV vector development in order to increase the efficiency of rAAV production. These strategies have all involved the use of adenovirus to provide the helper functions for rAAV production, however. Few studies have explored the possibility of using other helper viruses of AAV-2 replication and packaging for large-scale production.

In this paper, we report the development of an alternative system for production of rAAV. This system is based upon the HSV-1 helper functions of AAV-2 replication and packaging. By generating a recombinant HSV-1 encoding the AAV-2 *rep* and *cap* genes we have made a single infectious helper. The expression of Rep from this vector appears to be regulated and is appropriately distributed to the nucleus. The rHSV-1, *d27.1-rc*, propagates readily and its replication is not affected by the presence of *rep*.

Development of mature HSV-1 replication centers in the presence of *rep* appears to be unique to this vector. One possible explanation why the presence of the *rep* gene did not affect the kinetics of *d27.1-rc* replication or the formation of mature viral replication centers is that Rep proteins are not efficiently expressed in the V27 cells after *d27.1-rc* infection. Both Western analysis and an IFA were used to analyze Rep expression in 293, Vero and V27 cells after *d27.1-rc* infection. By Western analysis, high level Rep expression was observed in 293 cells and Vero cells but not in V27 cells after infection with *d27.1-rc* (Figure 2). By IFA, Rep expression was observed in the nucleus of infected 293 cells (Figure 3a) and Vero cells (data not shown) after infection with *d27.1-rc*, but not in V27 cells (Figure 4b). The minimal Rep expression after *d27.1-rc* infection of V27 cells may explain how generation of *d27.1-rc* was feasible and why similar efforts to construct recombinant Ad vectors with the *rep* gene have failed.

The *d27.1* vector was chosen as the mutant background to provide the viral helper functions for several reasons. The vector *d27.1* has a mutation in the immediate–early gene IE63 and does not produce ICP27.[31] The protein ICP27 has been implicated in the inhibition of host cell mRNA splicing.[47,48] The use of *d27.1* should minimize inhibition of splicing of the *rep* and *cap* messages compared with a vector which produces ICP27. In addition, *d27.1* overexpresses ICP8,[31] one of the HSV-1 genes essential for AAV-2 replication.[28] High-level expression of ICP8, the single-stranded DNA binding protein, should be beneficial for rAAV production.

The most efficient manner in which *d27.1-rc* can be used for large-scale rAAV production involves infection of a proviral cell line that provides the rAAV template to be packaged. In this two-component system, the proviral cell line could be grown at high densities in large quantities in spinner cultures or cartridge systems. The AAV-2 *rep* and *cap* genes and the helper functions required for rAAV production are then provided by *d27.1-rc* infection. Using *d27.1-rc* to infect the proviral cells would eliminate the need for transfection at any step in the production process. The choice of cell line used for this system is important, however. The results of Western analysis (Figure 2) indicate that *d27.1-rc* will efficiently express the AAV-2 Rep proteins only in certain cell lines.

The dose-response curve for the production of AAV-GFP by *d27.1-rc* demonstrates that increasing the MOI of *d27.1-rc* augments rAAV production to a point. The vector *d27.1-rc* still expresses the immediate–early genes that encode the viral proteins ICP0 and ICP4.[31] Expression of these immediate–early genes is detrimental to the cell and induces cell death.[49,50] At high MOIs, increased expression of these immediate–early genes probably leads to rapid cell death, limiting the production of rAAV. At a MOI of 25, while there is increased expression of the AAV-2 *rep* genes and the HSV-1 helper genes necessary for rAAV production, increased cytotoxicity due to additional gene expression from the vector also occurs. At a MOI of 10, the most effective balance exists between expression of the AAV-2 *rep* and *cap* genes and HSV-1 helper functions required for rAAV production and the cytotoxicity inherent to the vector.

Replication of HSV-1 is not required for efficient repli-

cation and packaging of AAV-2.[51] Cells lines such as 293 cells, which do not complement *d27.1-rc* replication, can therefore be used to produce rAAV. Using a non-complementing cell line to produce rAAV will permit the production of rAAV without generating additional *d27.1-rc*. The helper virus, *d27.1-rc*, will therefore be effectively eliminated from the rAAV produced.

The application of a recombinant virus to introduce the AAV-2 *rep* and *cap* and helper virus functions into cells to produce rAAV has many advantages over an amplicon system which we previously described.[32] Unlike a recombinant HSV-1 vector, an amplicon system has a variable helper virus to amplicon virus ratio from passage to passage. This variability makes optimization of an amplicon system for rAAV production difficult since the ratio of helper virus to amplicon virus will affect the amount of rAAV produced. In addition, there is no selective pressure to maintain the recombinant AAV-2 genome in the amplicon. With passage, deletion and recombination of the amplicon genome is likely to occur, resulting in decreased efficiency of rAAV production after serial passage of the amplicon. These problems are not encountered using the recombinant virus *d27.1-rc*.

Large-scale production of rAAV vectors will be required for *in vivo* preclinical and clinical trials of potentially therapeutic rAAV vectors. The vector *d27.1-rc* should facilitate the production of rAAV. The vector *d27.1-rc* is flexible and can be utilized to produce rAAV from transfected cells, cell lines or even infected rAAV. The rescue of rAAV from proviral cell lines at or above the efficiency of Ad-free methods will permit large-scale production of rAAV without requiring a transfection procedure. Combined with recently developed purification procedures (see accompanying article in this issue, pp 973–985), *d27.1-rc* will be an attractive way to produce the large quantity of rAAV that will be needed for clinical success of rAAV-based gene therapy.

Materials and methods

Plasmids

The plasmid pTR-UF5 is an AAV-GFP proviral construct with AAV-2 ITRs flanking both an eGFP and a neomycin resistance gene (*neo*) expression cassette. Expression of GFP is driven by the human CMV promoter. The *neo* gene is expressed from the HSV-1 *tk* promoter. The plasmid pSub201 contains the AAV-2 *rep* and *cap* genes and has previously been described.[16] The plasmid pHSV-106 is a pBR-derived plasmid into which the *Bam*HI fragment of HSV-1 (17+ stain) containing the thymidine kinase (*tk*) gene was cloned. The plasmid pHSV-106-*lacZ* was constructed by cloning a *lacZ* expression cassette into the *Kpn*I restriction site of pHSV-106 interrupting the *tk* gene. The plasmid pHSV-106-rc has the AAV-2 *rep* and *cap* genes from pSub201 cloned into the *Kpn*I site of pHSV-106.

Cell lines

The 293 and Vero cell lines were obtained from American Type Culture Collection (Rockville, MD, USA). The V27 cell line is a Vero-derived cell line that expresses the HSV-1 ICP27 protein and has previously been described.[31] The C12 cell line is a Hela-derived cell line with inducible AAV-2 *rep* gene expression and has been previously described.[22] The GFP-92 cell line was created by infecting 293 cells with AAV-GFP and has been previously described.[32] In AAV-GFP, expression of GFP is driven by the human CMV promoter and the *neo* gene is expressed from the HSV-1 *tk* promoter. All cell lines were maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum (FBS).

HSV-1 viruses

The virus *d27.1* is an ICP27 deletion mutant (Kos strain) which has been previously described and is propagated on the complementing cell line, V27.[31] The virus *d27.1-rc* was constructed by first creating the *lacZ* expressing virus *d27.1-lacZ*. The *lacZ* expressing vector was created by traditional techniques involving cotransfection of *d27.1* infected cell DNA and the integrating plasmid, pHSV-106-*lacZ* (linearized by *Bam*HI restriction digest) into V27 cells. Recombinant viruses were isolated by screening for blue plaques after agar overlay containing 400 μg/ml halogenated indolyl-β-D-galactoside (Bluogal; Gibco-BRL, Bethesda, MD, USA). Recombinant viruses were purified by three rounds of limiting dilution. Integration was confirmed by Southern analysis of restriction enzyme digested *d27.1-lacZ* infected cell DNA (data not shown). The virus *d27.1-rc* was created by cotransfection of *d27.1-lacZ* infected cell DNA and the *Sph*I linearized integration plasmid pHSV-106-rc into V27 cells. Recombinant viruses were isolated by screening for white plaques after agar overlay containing 400 μg/ml Bluo-gal. Recombinant viruses were purified by three rounds of limiting dilution. Integration was confirmed by Southern analysis of restriction enzyme digested *d27.1-rc* infected cell DNA (data not shown). The stability of integration with passage was assessed by isolating 10 clones of *d27.1-rc* after 10 serial passages of *d27.1-rc* at a MOI of 0.1. All clones were able to rescue rAAV (data not shown). Wild-type HSV-1 virus capable of replicating on Vero cells was not detected in any preparation (limit of detection is <20 plaque forming units (p.f.u.)/ml).

Recombinant AAV production methods

Production of AAV-GFP from pTR-UF5 transfected 293 cells: Tissue culture dishes (10 cm) plated with 2×10^6 293 cells were transfected with 5 μg pTR-UF5 and 25 μl Lipofectamine (Gibco-BRL) as per the manufacturer's instruction. Four hours after transfection, the cells were washed and DMEM (10% FBS) was added. Twenty hours later, the cells were superinfected with *d27.1-rc* at different MOIs or *d27.1-lacz* at a MOI of 10. (The cells on an extra transfected dish were trypsinized, resuspended and counted using a hemocytometer.) Approximately 3.5×10^7 cells were infected per MOI. Forty-eight hours later, the cells were harvested and pelleted by centrifugation (375 *g*, 5 min). The cells were then resuspended in 10 ml of DMEM and cell-associated rAAV was released by three rounds of freezing and thawing. Cell debris was pelleted by centrifugation (250 *g*, 5 min). The cell lysates were then titrated for EU of AAV-GFP as described below and purified by CsCl gradient as previously described.[1] This experiment was repeated in triplicate.

Production of AAV-GFP from the cell line GFP-92: The GFP-92 cells were plated in 75 cm^2 tissue culture flasks. Twelve hours later, the cells were infected with *d27.1-rc*

at different MOIs or *d27.1-lacz* at a MOI of 10. The number of cells in one extra flask was determined as described above. Approximately 1.5×10^7 GFP-92 cells were infected per MOI. Cells were harvested 48 h after infection and cell-associated AAV-GFP was processed and titered as described above. This experiment was repeated in triplicate.

Production of AAV-GFP by amplifying AAV-GFP via infection

293 Cells (1.5×10^6 cells) were plated in six-well tissue culture dishes. Twelve hours later, the cells were infected with AAV-GFP at different MOIs. Twelve hours later, the cells were infected with *d27.1-rc* at a MOI of 10. Cells were harvested 48 h after infection and cell-associated AAV-GFP was processed as described above. This experiment was repeated in triplicate. The amount of output rAAV was determined using the fluorescent cell assay described below.

Large-scale AAV-GFP production

GFP-92 cells were plated on 175 cm^2 tissue culture flasks 12 h before infection. 1×10^9 GFP-92 cells were infected 12 h later with *d27.1-rc* at a MOI of 10. Cells were harvested 48 h after infection and cell-associated AAV-GFP was processed as described above. This experiment was repeated in duplicate. Stocks were analyzed for replication-competent AAV (rcAAV) as previously described.[3] Replication-competent AAV was not detected (limit of detection was one replication unit per 10^7 GFP EU).

Titering of AAV-GFP in the cell lysates by the fluorescent cell assay

Cell lysates were heat inactivated (55°C, 1 h). Serial dilutions of AAV-GFP were then titered on C12 cells with Ad co-infection (MOI 20) as previously described.[52] The cells were then analyzed for GFP expression using fluorescence microscopy at 48 h after infection.

Western analysis of AAV-2 Rep proteins

The indicated cells (approximately 4×10^6 cells) were plated on to 6 cm tissue culture plates 12 h before infection with *d27.1-rc* (MOI as indicated). Control samples were not infected. Cells were harvested 48 h after infection and cell lysates were made and loaded on to a 10% sodium dodecyl sulfate (SDS)-polyacrylamide gel followed by immunoblotting using a monoclonal antibody (clone 1F11.8, 1:5000 dilution) that recognizes all four AAV-2 Rep proteins. The antibody was detected by chemiluminescence (Amersham, Arlington Heights, IL, USA).

Immunofluorescence assay

Cells (293, Vero or V27 cells) were plated on to two-well tissue culture slides at a density of 1.5×10^5 cells per well. For the anti-AAV Rep immunofluorescence assay, 293 cells were infected 12 h later with *d27.1-rc* at a MOI of 10. Cells were washed with DMEM after a 45 min adsorption period and DMEM with 10% FBS was then added. After 10 h, cells were washed twice with PBS and fixed for 10 min in 4% paraformaldehyde in PBS. Cells were washed twice with PBS and permeabilized with 0.2% Triton X-100 in PBS for 2 min. Cells were then washed twice with PBS and incubated for 1 h at 37°C in a humidified chamber with monoclonal anti-Rep antibody (American Research Products, Belmont, MA, USA, clone 226.7, 1:1 dilution). This antibody recognizes all four Rep proteins. The cells were then washed three times with PBS and incubated for 30 min at 37°C with FITC-conjugated, donkey anti-mouse secondary antibody (diluted 1:100 in 2% goat serum, 2% donkey serum in PBS). The slides were then washed three times, covered with a 4′, 6-diamidino-2- phenylindole (DAPI) containing mounting solution (Vector Laboratories, Burlingame, CA, USA), sealed and analyzed for immunofluorescence. Microscopy was performed on a Leitz microscope with Image Pro acquisition equipment and image analysis software.

To analyze the maturation of HSV-1 viral replication centers and Rep expression in V27 cells after *d27.1-rc* infection, a rabbit polyclonal anti-ICP8 (the HSV-1 single-stranded DNA binding protein) antibody (PAb 3–83) and the monoclonal anti-Rep antibody (American Research Products, clone 226.7, 1:1 dilution) were utilized in a double label experiment. All procedures were as previously described except that V27 cells were infected at a MOI of 1. After fixing and permeablization, V27 cells were incubated as above with the anti-Rep monoclonal antibody. The cells were then washed twice with PBS and incubated with the anti-ICP8 antibody (diluted 1:50 in 2% goat serum, 2% donkey serum in PBS) for 1 h in a humidified chamber at 37°C. The cells were then washed three times with PBS and incubated with a rhodamine-conjugated, donkey anti-rabbit secondary antibody and FITC-conjugated, donkey anti-mouse secondary antibody (both diluted 1:100 in 2% goat serum, 2% donkey serum in PBS) for 30 min at 37°C. The slides were then washed three times, covered with DAPI containing mounting solution, sealed and analyzed for immunofluorescence. (Vero cells were infected and processed alongside V27 cells to serve as positive controls for Rep staining.)

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(54) Title: METHODS FOR LARGE–SCALE PRODUCTION OF RECOMBINANT AAV VECTORS

(57) Abstract

Disclosed are HSV–1 amplicons that supply all necessary helper functions required for rAAV packaging and methods for their use. These HSV–1 amplicons have been shown to be capable of rescuing and replicating all forms of rAAV genomes including rAAV genomes introduced into cells by infection of rAAV virions, rAAV genomes transfected into cells on plasmids or proviral rAAV genomes integrated into cellular chromosomal DNA. Also provided are methods for preparing high–titer rAAV vector compositions suitable for gene therapy and the delivery of exogenous polynucleotides to selected host cells.

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DESCRIPTION

METHODS FOR LARGE-SCALE PRODUCTION OF RECOMBINANT AAV VECTORS

1.0 BACKGROUND OF THE INVENTION

The present application claims the priority date of co-pending provisional application Serial No. 60/101,507, filed September 22, 1998, the entire disclosure of which is incorporated herein by reference without disclaimer. The United States government has rights in the present invention pursuant to grant numbers CA28473 and CA09243 from the National Institutes of Health.

1.1 FIELD OF THE INVENTION

The present invention relates generally to the field of molecular biology. More particularly, it concerns the replication and packaging of recombinant adeno-associated viral-based vectors, and a scaleable process for their large-scale production.

1.2 DESCRIPTION OF RELATED ART

1.2.1 ADENO-ASSOCIATED VIRUS

Adeno-associated virus-2 (AAV)-2 is a human parvovirus that can be propagated both as a lytic virus and as a provirus (Cukor *et al.*, 1984; Hoggan *et al.*, 1972). The viral genome consists of linear single-stranded DNA (Rose *et al.*, 1969), 4679 bases long (Srivastava *et al.*, 1983), flanked by inverted terminal repeats of 145 bases (Lusby and Berns, 1982). For lytic growth AAV requires co-infection with a helper virus. Either adenovirus (Ad; Atchinson *et al.*, 1965; Hoggan, 1965; Parks *et al.*, 1967) or herpes simplex virus (HSV; Buller *et al.*, 1981) can supply the requisite helper functions. Without helper, there is no evidence of AAV-specific replication or gene expression (Rose and Koczot, 1972; Carter *et al.*, 1983). When no helper is available, AAV persists as an integrated provirus (Hoggan, 1965; Berns *et al.*, 1975; Handa *et al.*, 1977; Cheung *et al.*, 1980; Berns *et al.*, 1982).

Integration apparently involves recombination between AAV termini and host sequences and most of the AAV sequences remain intact in the provirus. The ability of AAV to integrate into host DNA is apparently an inherent strategy for insuring the survival of AAV sequences in the absence of the helper virus. When cells carrying an AAV provirus are subsequently superinfected with a helper, the integrated AAV genome is rescued and a productive lytic cycle occurs (Hoggan, 1965).

AAV sequences cloned into prokaryotic plasmids are infectious (Samulski *et al.*, 1982). For example, when the wild type AAV/pBR322 plasmid, pSM620, is transfected into human cells in the presence of adenovirus, the AAV sequences are rescued from the plasmid and a normal AAV lytic cycle ensues (Samulski *et al.*, 1982). This renders it possible to modify the AAV sequences in the recombinant plasmid and, then, to grow a viral stock of the mutant by transfecting the plasmid into human cells (Samulski *et al.*, 1983; Hermonat and Muzyczka, 1984).

AAV contains at least three phenotypically distinct regions (Hermonat and Muzyczka, 1984). The *rep* region codes for one or more proteins that are required for DNA replication and for rescue from the recombinant plasmid, while the *cap* and *lip* regions appear to code for AAV capsid proteins and mutants within these regions are capable of DNA replication (Hermonat and Muzyczka, 1984). It has been shown that the AAV termini are required for DNA replication (Samulski *et al.*, 1983).

The construction of two *E. coli* hybrid plasmids, each of which contains the entire DNA genome of AAV, and the transfection of the recombinant DNAs into human cell lines in the presence of helper adenovirus to successfully rescue and replicate the AAV genome has been described (Laughlin *et al.*, 1983; Tratschin *et al.*, 1984a; 1984b).

1.2.2 rAAV Vectors as Vehicles for Gene Therapy

Recombinant adeno-associated virus (rAAV) vectors have important utility as vehicles for the *in vivo* delivery of polynucleotides to target host cells (Kessler *et al.*, 1996; Koeberl *et al.*, 1997; Kotin, 1994; Xiao *et al.*, 1996). rAAV vectors are useful vector for efficient and long-term gene transfer in a variety of mammalian tissues,

e.g., lung (Flotte, 1993), muscle (Kessler, 1996; Xiao *et al.*, 1996; Clark *et al.*, 1997; Fisher *et al.*, 1997), brain (Kaplitt, 1994; Klein, 1998) retina (Flannery, 1997; Lewin *et al.*, 1998), and liver (Snyder, 1997).

It has also been shown that rAAV can evade the immune response of the host by failing to transduce dendritic cells (Jooss *et al.*, 1998). Clinical trials have been initiated for several important mammalian diseases including hemophilia B, muscular dystrophy and cystic fibrosis (Flotte *et al.*, 1996; Wagner *et al.*, 1998).

1.2.3 Contemporary Methods for Preparing rAAV Vectors

Currently, rAAV is most often produced by co-transfection of rAAV vector plasmid and wt AAV helper plasmid into Ad-infected 293 cells (Hermonat and Muzyczka, 1984). Recent improvements in AAV helper design (Li *et al.*, 1997) as well as construction of non-infectious mini-Ad plasmid helper (Grimm *et al.*, 1998; Xiao *et al.*, 1998; Salvetti, 1998) have eliminated the need for Ad infection, and made it possible to increase the yield of rAAV up to 10^5 particles per transfected cell in a crude lysate. Scalable methods of rAAV production that do not rely on DNA transfection have also been developed (Chiorini *et al.*, 1995; Inoue and Russell, 1998; Clark *et al.*, 1995). These methods, which generally involve the construction of producer cell lines and helper virus infection, are suitable for high-volume production.

The conventional protocol for downstream purification of rAAV involves the stepwise precipitation of rAAV using ammonium sulfate, followed by two or preferably, three rounds of CsCl density gradient centrifugation. Each round of CsCl centrifugation involves fractionation of the gradient and probing fractions for rAAV by dot-blot hybridization or by PCR™ analysis.

1.3 Deficiencies in the Prior Art

A major problem associated with the use of rAAV vectors has been the difficulty in producing large quantities of high-titer vector stocks (Clark *et al.*, 1995, Clark *et al.*, 1996). The standard production protocol involves low-efficiency transfection of plasmid DNA containing the *rep* and *cap* genes and a plasmid

containing the rAAV provirus with inverted terminal repeats. Cells are then superinfected with adenovirus to provide essential helper functions required for rAAV production.

Alternative procedures have been developed to improve the efficiency of rAAV production by delivering *rep*, *cap* and the adenovirus helper genes. These technologies have included the generation of *rep* and *cap* inducible cell lines and plasmids expressing the essential adenovirus helper genes (Clark *et al.*, 1995; Clark *et al.*, 1996; Vincent *et al.*, 1990; Xiao *et al.*, 1998; Grimm *et al.*, 1998). Although these techniques have improved the yield of rAAV production, they have not been entirely satisfactory. Procedures employing transfection methods are not efficient, and tend to be extremely variable in yield from preparation to preparation. Moreover, such procedures are difficult to scale up to produce the large quantity of rAAV vector needed for clinical trials.

The production of *rep* and *cap* inducible cell lines is a particular challenge because the yield of rAAV produced from different clones is variable and does not exceed the efficiency of transfection methods (Clark *et al.*, 1995; Clark *et al.*, 1996, Vincent *et al.*, 1990). Production procedures for rAAV that utilize adenovirus and transfection of *rep* and *cap* containing plasmids have the potential to generate wild type AAV (wt AAV) through illegitimate recombination of the ITRs with *rep* and *cap* sequences. This leads to preferential amplification of the wt AAV genome over the rAAV genome.

A major drawback in the use of rAAV vectors for gene transfer studies *in vivo* and their application to clinical procedures, such as that of gene therapy, has been the difficulty in producing large quantities of rAAV vector. For the therapeutic correction of some diseases, it is estimated that 1×10^{14} rAAV particles must be administered per patient. This will require the culture of greater than 1×10^{12} cells to produce the quantity of rAAV vector that will be needed to therapeutically treat each patient. The use of contemporary transfection methods on this scale of rAAV production is extremely problematic, costly and time consuming.

The development of a packaging system that provides all the helper functions needed for rAAV production from a rAAV producer cell line would greatly facilitate the large-scale production of rAAV. Transfection procedures would not be required and the producer cell line could be grown in large quantities at high densities in commercially available laboratory equipment.

2.0 SUMMARY OF THE INVENTION

The present invention overcomes these and other inherent limitations in the prior art by providing packaging systems that provide all of the required helper functions, and methods for the large-scale production of rAAV. The present invention demonstrates the ability of a recombinant herpes simplex virus (rHSV) or a rHSV amplicon expressing AAV Rep and Cap to support replication and packaging of rAAV. The present methods overcome the need for transfection procedures, and provide reliable, cost-effective means for generating large quantities of rAAV. Superinfection of appropriate host cell cultures with the vectors described herein produces quantities of rAAV not attainable by any other means. By providing a second virus or cell line that contains the rAAV provirus, the present methods overcome the significant problem of spontaneous deletions in the AAV ITR when growing rAAV-based plasmids in bacterial cell cultures.

The present invention provides the first system that supplies AAV genes *rep* and *cap* and the HSV-1 helper functions needed for rAAV production in one delivery vehicle. The rHSV-1 and rHSV-1 amplicon-based vector systems supply Rep, Cap and the HSV-1 helper functions required for rAAV production. Amplicon and virus stocks have been produced that express Rep and Cap from their native promoters (p5, p19 and p40). To increase the yield of rAAV production and make the rHSV-1 and rHSV-1 amplicon systems practical alternatives to adenoviral systems for rAAV production, HSV-1 amplicon and vector systems that expresses Rep and Cap from their native promoters and uses an ICP27 mutated HSV-1 virus, d27-1, as the genetic background of the amplicon or vector has been developed. Use of the defective HSV-1 amplicon or vector results in rAAV production with an efficiency that exceeds

previously described methods (Flotte *et al.*, 1995). Southern blot and PCR™ analyses have shown that no wt AAV were produced using these modified amplicons or helper viruses. The present system provides means for increasing the scale of rAAV production to a level such that sufficient rAAV can now be produced for preclinical and clinical trials utilizing rAAV-based vectors for gene delivery.

The present invention provides DNA segments comprising an AAV *rep* coding sequence operably linked to a promoter, an AAV *cap* coding sequence operably linked to a promoter, an HSV-1 origin of replication and an HSV-1 packaging sequence. In preferred embodiments, the AAV *rep* coding sequence and/or the AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter. In certain embodiments, the DNA segment is comprised within a recombinant herpes simplex virus vector, or within a recombinant herpes simplex virus capsid.

As used herein in this context, the term "recombinant herpes simplex virus vector" will be understood to mean genomic DNA of the herpes simplex virus with non-herpes simplex virus DNA added by the hand of man. The term "recombinant herpes simplex virus capsid", as used herein in this context will be understood to mean the herpes simplex virus head, comprised of herpes simplex virus capsid proteins, comprising a recombinant DNA segment, such as a plasmid, cosmid or the like, that comprises at least an HSV-1 origin of replication and an HSV-1 packaging sequence.

Thus, the present invention also provides recombinant herpes simplex virus vectors comprising an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter. In preferred aspects of the invention, the AAV *rep* coding sequence and/or the AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

In certain recombinant herpes simplex virus vectors of the present invention, a non-essential HSV gene is altered. In particular embodiments, the non-essential HSV gene is altered to increase expression. In a general sense, genes that encode proteins that are beneficial to the host cell, or that increase the production of rAAV particles are contemplated for such alteration. Examples of non-essential HSV genes that are

altered to increase expression includes, but is not limited to, the HSV gene encoding ICP8.

In other embodiments, the non-essential HSV gene is mutated, such as by one or more point mutants or insertions, or substantially or completely deleted, such that the gene product of the non-essential HSV gene is either non-functional or absent. In a general sense, genes that encode proteins that are deleterious to the host cell, or that decrease the production of rAAV particles are contemplated for such alteration. Examples of non-essential HSV genes that are contemplated for mutation or deletion include, but are not limited to, the HSV genes encodes ICP27, an HSV late gene and/or glycoprotein H.

In preferred embodiments of the invention, the recombinant vector is comprised within a recombinant herpes simplex virus. As used herein in his context, the term " recombinant herpes simplex virus" will be understood to mean a complete herpes simplex virus that comprises a "recombinant herpes simplex virus vector", as defined above.

Therefore, the present invention further provides recombinant herpes simplex viruses comprising an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter. In preferred aspects of the invention, the AAV *rep* coding sequence and/or the AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

In certain recombinant viruses of the present invention, a non-essential HSV gene is altered. In particular embodiments, the non-essential HSV gene is altered to increase expression. Examples of non-essential HSV genes that are altered to increase expression includes, but is not limited to, the HSV gene encoding ICP8. In other embodiments, the non-essential HSV gene is mutated, such as by one or more point mutants or insertions, or substantially or completely deleted, such that the gene product of the non-essential HSV gene is either non-functional or absent. Examples of non-essential HSV genes that are contemplated for mutation or deletion include, but are not limited to, the HSV genes encodes ICP27, an HSV late gene and/or glycoprotein H. In preferred embodiments, the recombinant virus is the *d27.1rc* virus.

The present invention also provides kits comprising, in a suitable container, a DNA segment comprising an AAV *rep* coding sequence operably linked to a promoter, an AAV *cap* coding sequence operably linked to a promoter, an HSV-1 origin of replication and an HSV-1 packaging sequence. In further aspects of the invention, the kit comprises an HSV-1 helper virus. In preferred aspects, a non-essential gene of the HSV-1 helper virus is altered. As detailed above, in certain aspects of the invention, a non-essential gene of the HSV-1 helper virus, exemplified by, but not limited to the gene encoding ICP8, is altered to increase expression. In other aspects, a non-essential gene of the HSV-1 helper virus, including, but not limited to the genes encoding ICP27 and/or glycoprotein H, is mutated or substantially deleted. In certain preferred embodiments, the HSV-1 helper virus is the d27.1 HSV-1 virus.

Additionally, the present invention provides kits comprising, in a suitable container, a recombinant herpes simplex virus vector comprising an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter. In preferred kits of the invention, the recombinant herpes simplex virus vector is comprised in a recombinant herpes simplex virus.

The present invention also provides methods for preparing a rAAV comprising providing an HSV-1 helper virus and a DNA segment comprising an AAV *rep* coding sequence operably linked to a promoter, an AAV *cap* coding sequence operably linked to a promoter, an HSV-1 origin of replication and an HSV-1 packaging sequence to a host cell that comprises a rAAV, culturing the cell under conditions effective to produce rAAV in the cell, and obtaining the rAAV from the cell. As used herein in this context, the term "host cell that comprises a rAAV" will be understood to include a host cell that comprises a rAAV provirus integrated into the genome of the host cell, as well as a host cell that is infected with a rAAV. Thus, in certain aspects, the host cell comprises the rAAV integrated into the genome of the cell, while in other aspects the host cell is provided with the rAAV, the HSV-1 helper virus and the DNA segment simultaneously.

Preferred host cells include, but are not limited to, HeLa, 293 or Vero cells. In certain preferred methods of the invention, the rAAV comprises an AAV-2 genome. However, while the preferred rAAV genome is generally the AAV-2 genome, the capsid can be from any serotype of AAV. Therefore, in particular methods, the rAAV comprises an AAV-1, AAV-2, AAV-3, AAV-4, AAV-5 or AAV-6 capsid. As the present compositions and methods are designed for large-scale production of rAAV vectors, in preferred embodiments, the rAAV comprises a therapeutic gene. In certain methods, the AAV *rep* coding sequence and/or the AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter. In other methods, at least a first AAV capsid protein is operably linked to an HSV late promoter, such as the HSV 110 promoter.

As detailed above, in certain methods of the present invention a non-essential gene of the HSV-1 helper virus is altered. In certain methods, a non-essential gene of the HSV-1 helper virus, exemplified by, but not limited to the gene encoding ICP8, is altered to increase expression. In other methods, a non-essential gene of the HSV-1 helper virus, including, but not limited to the genes encoding ICP27 and/or glycoprotein H, is mutated or substantially deleted. In certain preferred methods, the HSV-1 helper virus is the d27.1 HSV-1 virus. Thus, the present invention further provides a recombinant AAV virus produced by any of the methods of the present invention, as well as kits comprising, in a suitable container, a recombinant AAV virus produced by any of the methods of the present invention.

The present invention additionally provides methods for preparing a rAAV comprising providing a recombinant herpes simplex virus that comprises an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter to a host cell that comprises a rAAV, culturing the cell under conditions effective to produce rAAV in the cell, and obtaining the rAAV from the cell.

As detailed above, in certain methods a non-essential gene of the recombinant herpes simplex virus, such as the gene encoding ICP8, is altered to increase expression, while in other methods, a non-essential gene of the recombinant herpes

simplex virus, such as the gene encoding ICP27 or glycoprotein H, is mutated or substantially or completely deleted.

3.0 BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1 shows a map of pHSV-RC, which was used to generate amplicons that replicate and package rAAV virions. The plasmid is a pUC-based vector. The *a*-sequence contains the HSV-1 packaging signals and is cloned into the *Eco*RI site. The *110*- sequence contains an HSV-1 origin of replication and is the internal *Sma*I fragment from the HSV-1 *ori S*. The *110*-sequence is inserted in the *Sma*I site. (The *110* and *a*-sequence containing plasmid is p110a.) *Rep* and *cap* are the AAV-2 *rep* and *cap* genes isolated from psub201 by an *Xba*I digest and cloned into the *Xba*I site of p110a to create pHSV-RC.

FIG. 2 shows the integration vector used to produce *d27.1-rc*. The plasmid pHSV-106 contains the *BamH*I fragment encoding the *tk* gene of HSV-1. The AAV-2 *rep* and *cap* genes, under control of their native promoters, were cloned into the *Kpn*I site of *tk* gene to generate pHSV-106-rc. Restriction digest of pHSV-106-rc with *Sph*I was used to generate the linear fragment. This fragment was cotransfected with *d27.1-lacZ* infected cell DNA into V27 cells to generate *d27.1-rc* by homologous recombination.

FIG. 3 demonstrates that recombinant adeno-associated virus can be amplified after coinfection with *d27.1-rc*. 293 cells were transfected with AAV-GFP proviral plasmid. Approximately $3x10^7$ cells were present in each group. 24 h after transfection, the cells were superinfected with different MOIs of *d27.1-rc*. 36 h post infection, a cell lysate was made from the infected cells by three rounds of freeze-thaw. The viral lysate was heat inactivated at 55°C for one hour and then titered in duplicate on C12 cells that were coinfected with Ad (MOI of 20). 48 h post infection

the C12 cells were analyzed for GFP expression using fluorescent microscopy and a titer was determined (in expression units). The amount of AAV-GFP produced per transfected cell was then calculated. This study was repeated three times.

FIG. 4 illustrates that the vector *d27.1-rc* can produce rAAV from a proviral cell line. The cell line GFP-92 is a 293 derived cell line that has a single copy of AAV-GFP integrated into its genome. The vector *d27.1-rc* was used to produce AAV-GFP from this cell line. $1.5x10^7$ GFP-92 cells were infected with *d27.1-rc* at different MOIs. 48h post-infection a cell lysate was made from the infected cells by three rounds of freeze-thaw. The viral lysate was heat inactivated at 55°C for one hour and then titered in duplicate on C12 cells that were coinfected with Ad (MOI of 20). 48h post-infection the C12 cells were analyzed for GFP expression using fluorescent microscopy and a titer was determined (expression units). The amount of AAV-GFP produced per transfected cell was then calculated. This study was repeated three times.

4.0 DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

4.1 CONSTRUCTION OF MODIFIED GENE THERAPY VECTORS

Amplicons and viral vectors have been constructed that contain the AAV *rep* and *cap* genes under control of their native promoters (p5, p19 and p40). HSV-1 amplicons and viral vectors (HSV-RC/KOS, HSV-RC/d27 and HSV-AAV-GFP) were generated by supplying helper functions with either wild type HSV-1 (KOS strain) or the ICP27 immediate early mutant of HSV-1, d27-1, respectively, by homologous recombination using the targeting vector shown in FIG. 2. Growth of the amplicon or recombinant virus stock is not inhibited in the presence of Rep protein, which highlights important differences between HSV-1 and adenovirus (Ad) replication and the mechanism of providing helper function for productive AAV infection. Co-infection of rAAV and HSV-RC/d27 (also termed *d27.1rc*) results in the replication and amplification of rAAV genomes.

Similarly, rescue and replication of rAAV genomes are possible when recombinant vector plasmids were transfected into cells followed by *d27.1rc*

infection. Production of infectious rAAV by rescue from two rAAV producer cell lines has also been achieved using both HSV-RC/KOS and HSV-RC/d27. The titer of rAAV produced using HSV-RC/d27 is similar to that achieved by supplying *rep* and *cap* by the most efficient transfection method developed utilizing adenovirus. Importantly, no detectable wild type AAV is generated using this approach. These results demonstrate that rHSV amplicons and vectors expressing the AAV *rep* and *cap* genes support the replication and packaging of rAAV vectors in a scaleable process, allowing for large-scale production of vector.

The HSV-RC/KOS and HSV-RC/d27 amplicons were able to replicate and amplify all forms of proviral rAAV. These amplicons are useful in replication center assays and also for the detection of episomal or integrated proviral rAAV in cells previously infected with rAAV. While the amplicon demonstrates the ability of rHSV to replicate in the presence of rAAV, there is an advantage to having a single recombinant molecule that expresses rep and cap. Therefore, the rHSV, *d27.1-rc* was generated as described below.

The use of HSV-RC/KOS or HSV-RC/d27 eliminates the need for coinfection of cells with wild-type (wt) AAV and adenovirus, and helps standardize problematic assays, which are difficult to reproduce. Eliminating the use of wt AAV is also desirable since it reduces the likelihood of wt AAV contamination of viral preparations and cells.

A producer cell line was able to produce rAAV vector when infected with HSV-RC/KOS. However, although HSV-RC/KOS could express all of the helper functions needed for rAAV production, this system was extremely inefficient. A defective HSV-1 vector, d27-1, which overexpresses the HSV-1 helper genes required for AAV replication, was then used to make the second Rep and Cap expressing amplicon, HSV-RC/d27. The HSV-RC/d27 alone was shown to be capable of providing all of the helper functions required for rAAV replication and packaging. Infection with HSV-RC/d27 was capable of producing rAAV particles as efficiently as transfection methods. Infection with HSV-RC/d27 followed by HSV-1 superinfection was able to produce rAAV particles more efficiently than transfection

methods. The rAAV virus produced by the HSV-1 amplicons was infectious after heat inactivation and CsCl gradient purification. Finally, wt AAV was not detected in any of the HSV-1 amplicon produced rAAV preparations.

4.2 Large-Scale Production of Modified Gene Therapy Vectors

Purification of rAAV intended for clinical trials will be facilitated by the disclosed amplicons and viral vectors. HSV-1 is a large enveloped virus greater than 200 nm in diameter (Roizman and Sears, 1996). The HSV-1 virion is extremely sensitive to heat and chemical inactivation. Additionally, size exclusion chromatography is extremely effective at eliminating HSV-1 virions from the rAAV preparations. This is likely due to the large size difference between the AAV capsid (20 nm diameter) and HSV-1 virion. Chromatographic methods have been developed to increase the efficiency of rAAV production by eliminating the need for CsCl gradients (Tamayose *et al.*, 1997). Size exclusion chromatography may be easily be added to these production processes.

The present invention allows for the large-scale growth of host cells that contain infectious rAAV particles. In general, approximately 10^{11} to 10^{12} cells, each containing approximately 500 infectious particles per cell, are needed for the production of sufficient rAAV particles for use in gene therapy of patients. Previously, the growth of this number of cells would have taken approximately one year. Using the methods disclosed herein, the time need to grow this number of host cells can be reduced to as little as two weeks or so. Large scale growth of host cells for rAAV production can be facilitated using the methods disclosed herein, and modern apparatus for cell growth, such as that disclosed in U.S. Patent 5,501,971, incorporated herein by reference in its entirety.

Substitution of heterologous promoters such as the HIV LTR or the HCMV IE promoter to drive Rep or Cap expression has been shown to increase the production of rAAV in transfection systems (Flotte *et al.*, 1995; Vincent *et al.*, 1997a). Constructs where Rep and Cap are expressed from these promoters are easily incorporated into the amplicon plasmid. Alternatively, one may use HSV-1 viral promoters

incorporating VP16 responsive elements such as the HSV-1 IE-110 promoter to drive *cap* expression. The transactivating properties of the HSV-1 virion factor VP-16 would increase Cap expression, and increase rAAV production. Amplification of rAAV virions from a cell lysate using an HSV-1 amplicon system is also contemplated, eliminating the need for proviral cell lines and large-scale transfections. Stepwise coinfections may then be utilized to amplify the quantity of rAAV vector as is commonly done for other recombinant viruses that replicate in complementing cell lines.

Clearly, Rep does not disrupt HSV-1 replication as completely as it does adenovirus replication. One member of the herpes virus family, HHV-6, actually encodes and expresses a functional Rep homologue (Thomson and Efstathiou, 1991; Thomson *et al.*, 1994). In contrast, Rep potently disrupts the replication of adenovirus and has made the production of p5 driven *rep* recombinant Ad unsuccessful to date. The creation of inducible promoter driven *rep* recombinant adenoviruses has also been problematic. While Rep has been shown to decrease HSV-1 viral DNA replication, it clearly does not preclude construction of amplicons, which express a functional Rep.

AAV-2 infection results in the AAV-2 genome entering a non-productive, non-progeny producing latent state where the viral genome exists as a provirus integrated into the host cell's chromosomal DNA (Cheung *et al.*, 1980). Preferential integration of the wt AAV genome seems to occur *via* site specific, nonhomologous recombination in human cells at chromosome 19q13.3 (Kotin and Berns, 1989; Kotin *et al.*, 1992; Kotin *et al.*, 1990; Samulski *et al.*, 1991). A productive lytic cycle ensues in which AAV DNA is replicated, amplified and packaged into progeny virions only during coinfection of AAV with the appropriate helper virus (adenovirus or herpes viruses) or infection of a latently infected cell with helper virus (Berns *et al.*, 1988; Russell *et al.*, 1995). Infection of wt AAV in the presence of DNA damaging agents also promotes viral replication through the induction of cellular DNA repair pathways.

The AAV DNA sequences, AAV viral proteins and helper virus genes that are required for productive wt AAV infection have been identified and have been utilized

to produce rAAV vectors (Berns, 1984; Carter, 1990; Huang and Hearing, 1989; Mishra and Rose, 1990; Samulski and Shenk, 1988; Weindler and Heilbronn, 1991). The DNA sequences required for AAV replication that serve as origins of replication of the AAV genome and primers of second strand synthesis are located in the inverted terminal repeats (ITRs) of the AAV genome (Samulski *et al.*, 1983). These sequences must be located *cis* to the recombinant genome that is to be replicated and packaged, and this rAAV genome is usually introduced into cells by transfection. The AAV Rep 78 or Rep 68 proteins, which direct replication of the genome from the ITRs, the viral Rep 52 and 40, which are necessary for efficient packaging, and the structural capsid proteins VP1, VP2 and VP3, are supplied in trans in the traditional packaging scheme, usually by transfection of Rep and Cap expressing plasmids (Samulski *et al.*, 1987). Viral helper functions for AAV replication are usually supplied by adenoviral early gene expression of E1a, E1b, E2a, E4 and by VA RNA after adenovirus infection (Berns, 1984; Carter, 1990; Huang and Hearing, 1989; Samulski and Shenk, 1988).

Adenovirus has been the most thoroughly studied AAV helper virus, and the virus generally utilized to produce rAAV. The adenovirus helper functions required for AAV-2 or rAAV replication are probably not involved in AAV DNA synthesis directly. Instead, the adenoviral helper genes make AAV replication possible through regulation of cellular gene expression and regulation of *rep* expression (Im and Muzyczka, 1990). Attempts to use Ad vectors to carry AAV genes have met with failure, presumably because the AAV *rep* gene is not tolerated by Ad.

Like adenovirus, HSV-1 is a fully competent helper virus for wt AAV replication and packaging (Johnston *et al.*, 1997; Mishra and Rose, 1990; Weindler and Heilbronn, 1991). In contrast to adenovirus, however, the helper functions provided by HSV-1 are due to the activities of replication proteins and not transcriptional regulators (Weindler and Heilbronn, 1991). The minimal set of HSV-1 genes required for efficient AAV replication and encapsidation include UL5, UL8, UL52 and UL29 (Weindler and Heilbronn, 1991). The genes UL5, UL8, and UL52 encode components of the HSV-1 helicase-primase complex (Crute *et al.*, 1989). UL29 encodes a single-stranded DNA binding protein (Knipe *et al.*, 1982). These

four proteins essential for AAV DNA replication are components of the HSV-1 core replication machinery along with the HSV-1 DNA polymerase (UL30), the polymerase-accessory factor (UL42) and the origin binding protein (UL9) (Challberg, 1986; Wu *et al.*, 1988). The genes UL5, UL8, UL52, and UL29 are transcribed early in infection preceding HSV-1 DNA replication and are absolutely required for HSV-1 DNA replication (Roizman and Sears, 1996). AAV replication and packaging can occur in the absence of HSV-1 DNA replication as long as HSV-1 early gene expression occurs (Weindler and Heilbronn, 1991).

4.3 Incorporation of rAAV Vectors Into Cells

In various embodiments of the invention, DNA is delivered to a cell as an expression construct. Preferred gene therapy vectors of the present invention are generally viral vectors.

Adeno-associated virus (AAV) is particularly attractive for gene transfer because it does not induce any pathogenic response and can integrate into the host cellular chromosome (Kotin *et al.*, 1990). The AAV terminal repeats (TRs) are the only essential *cis*-components for the chromosomal integration (Muzyczka and McLaughin, 1988). These TRs are reported to have promoter activity (Flotte *et al.*, 1993). They may promote efficient gene transfer from the cytoplasm to the nucleus or increase the stability of plasmid DNA and enable longer-lasting gene expression. Studies using recombinant plasmid DNAs containing AAV TRs have attracted considerable interest. AAV-based plasmids have been shown to drive higher and longer transgene expression than the identical plasmids lacking the TRs of AAV in most cell types (Shafron *et al.*, 1998).

AAV (Ridgeway, 1988; Hermonat and Muzyczka, 1984) is a parovirus, discovered as a contamination of adenoviral stocks. It is a ubiquitous virus (antibodies are present in 85% of the US human population) that has not been linked to any disease. It is also classified as a dependovirus, because its replication is dependent on the presence of a helper virus, such as adenovirus. Five serotypes have been isolated, of which AAV-2 is the best characterized. AAV has a single-stranded

linear DNA that is encapsidated into capsid proteins VP1, VP2 and VP3 to form an icosahedral virion of 20 to 24 nm in diameter (Muzyczka and McLaughlin, 1988).

The AAV DNA is approximately 4.7 kilobases long. It contains two open reading frames and is flanked by two ITRs. There are two major genes in the AAV genome: *rep* and *cap*. The *rep* gene encodes a protein responsible for viral replication, whereas *cap* encodes the capsid protein, VP1-3. Each ITR forms a T-shaped hairpin structure. These terminal repeats are the only essential *cis* components of the AAV for chromosomal integration. Therefore, the AAV can be used as a vector with all viral coding sequences removed and replaced by the cassette of genes for delivery. Three viral promoters have been identified and named p5, p19, and p40, according to their map position. Transcription from p5 and p19 results in production of Rep proteins, and transcription from p40 produces the Cap proteins (Hermonat and Muzyczka, 1984).

There are several factors that prompted researchers to study the possibility of using rAAV as an expression vector. One is that the requirements for delivering a gene to integrate into the host chromosome are surprisingly few. It is necessary to have the 145-bp ITRs, which are only 6% of the AAV genome. This leaves room in the vector to assemble a 4.5-kb DNA insertion. AAV is also a good choice of delivery vehicles due to its safety. There is a relatively complicated rescue mechanism: not only wild type adenovirus but also AAV genes are required to mobilize rAAV. Likewise, AAV is not pathogenic and not associated with any disease. The removal of viral coding sequences minimizes immune reactions to viral gene expression, and therefore, rAAV does not evoke an inflammatory response. AAV therefore, represents an ideal candidate for delivery of the present hammerhead ribozyme constructs.

Retroviruses have promise as gene delivery vectors due to their ability to integrate their genes into the host genome, transferring a large amount of foreign genetic material, infecting a broad spectrum of species and cell types and of being packaged in special cell-lines.

Of course, in using viral delivery systems, one will desire to purify the virion sufficiently to render it essentially free of undesirable contaminants, such as defective interfering viral particles or endotoxins and other pyrogens such that it will not cause any untoward reactions in the cell, animal or individual receiving the vector construct. A preferred means of purifying the vector involves the use of buoyant density gradients, such as cesium chloride gradient centrifugation, heparin affinity chromatography (Clark *et al.*, 1999), or non-ionic iodixinol gradients followed by heparin affinity chromatography (Zolotukhin *et al.*, 1999).

The titer of AAV in a given sample may be determined using any one of the methods routinely accepted in the AAV arts. For example, the inventors routinely use the methods of QC-PCR™ or infectious center assay, as described in detail in the Examples and by Zolotukhin *et al.* (1999), to determine the titer of a viral stock.

Likewise, the infectivity of a given AAV sample may be determined using any one of the methods routinely accepted in the AAV arts. For example, the inventors routinely use the methods of Hermonat and Muzyczka (1984) or Clark *et al.* (1999) to determine the infectivity of a given AAV stock.

The titer and infectivity of HSV in a given sample may also be determined using any one of the conventional methods known to those of skill in the art. For example, the methods described in detail in Example 9, below, are routinely employed by the inventors to determine the titer and infectivity of an HSV viral stock. Infectivity and titer are equivalent for HSV, since plaque-forming units are measured.

4.4 HERPES SIMPLEX VIRUS

As described in U.S. Patent 5,879,934 (specifically incorporated herein by reference in its entirety), Herpes simplex virus (HSV) comprises a double-stranded, linear DNA genome that encodes approximately 80 genes and consists of an approximately 152-kb nucleotide sequence. The viral genes are transcribed by cellular RNA polymerase II and are temporally regulated, resulting in the transcription and subsequent synthesis of gene products in roughly three discernable phases. These phases are referred to as the Immediate Early (IE, or α), Early (E, or β) and Late (L, or

γ) genes. Immediately following the arrival of the genome of a virus in the nucleus of a newly infected cell, the IE genes are transcribed. The efficient expression of these genes does not require prior viral protein synthesis. The products of IE genes are required to activate transcription and regulate the remainder of the viral genome.

One IE protein, Infected Cell Polypeptide 4 (ICP4), also known as α4, or Vmw175, is absolutely required for both virus infectivity and the transition from IE to later transcription (DeLuca *et al.*, 1987; DeLuca *et al.*, 1988; Paterson *et al.*, 1988a; 1988b; Shepard *et al.*, 1989; Shepard *et al.*, 1991).

U. S. Patent 5,879,934 teaches that several reports have described the use of viruses deleted in ICP4 for gene transfer (Breakefield *et al.*, 1991; Chocca *et al.*, 1990). One property of viruses deleted for ICP4 that makes them desirable for gene transfer is that they only express the five other IE genes: ICP0, ICP6, ICP27, ICP22 and ICP47 (DeLuca *et al.*, 1985). This excludes the expression of viral genes encoding proteins that direct viral DNA synthesis, as well as the structural proteins of the virus, which is desirable because it minimizes possible deleterious effects on host cell metabolism following gene transfer.

4.5 Methods of Nucleic Acid Delivery and DNA Transfection

In some embodiments, it may be desirable to use other methods for the transfer of expression constructs into target mammalian cells. Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use, as discussed below. Likewise, in some applications, it may be desirable to transfer a naked DNA expression construct into cells using methods such as particle bombardment. This method depends on the ability to accelerate DNA coated microprojectiles to a high velocity allowing them to pierce cell membranes and enter cells without killing them. Several devices for accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides the motive force. The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

In certain embodiments, it is contemplated that one or more polynucleotide compositions disclosed herein will be used to transfect an appropriate host cell. Technology for introduction of nucleic acids into cells is well known to those of skill in the art. These include calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe *et al.*, 1990) DEAE-dextran (Gopal, 1985), electroporation (Wong and Neumann, 1982; Fromm *et al.*, 1985; Tur-Kaspa *et al.*, 1986; Potter *et al.*, 1984; Suzuki et al., 1998; Vanbever *et al.*, 1998), direct microinjection (Capecchi, 1980; Harland and Weintraub, 1985), DNA-loaded liposomes (Nicolau and Sene, 1982; Fraley *et al.*, 1979; Takakura, 1998) and lipofectamine-DNA complexes, cell sonication (Fechheimer *et al.*, 1987), gene bombardment using high velocity microprojectiles (Yang *et al.*, 1990; Klein *et al.*, 1992), and receptor-mediated transfection (Curiel *et al.*, 1991; Wagner *et al.*, 1992; Wu and Wu, 1987; Wu and Wu, 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

4.6 Liposome and Nanocapsule Formulations

In a further embodiment of the invention, the rAAV vectors and related expression constructs may be formulated by entraping within a liposome, nanocapsule, microcapsule, lipofectamine-DNA complex, or other suitable lipid particle, as discussed below. In certain embodiments, the inventors contemplate the use of liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for the introduction of the viral compositions of the present invention into suitable host cells.

Liposome-mediated nucleic acid delivery and expression of foreign DNA *in vitro* has been very successful. Wong *et al.* (1980) demonstrated the feasibility of liposome-mediated delivery and expression of foreign DNA in cultured chick embryo, HeLa and hepatoma cells. In certain embodiments of the invention, the liposome may be complexed with a hemagglutinating virus (HVJ). This has been shown to facilitate fusion with the cell membrane and promote cell entry of liposome-encapsulated DNA. In other embodiments, the liposome may be complexed or employed in conjunction

with nuclear non-histone chromosomal proteins (HMG-1). In yet further embodiments, the liposome may be complexed or employed in conjunction with both HVJ and HMG-1. In other embodiments, the delivery vehicle may comprise a ligand and a liposome.

Such formulations may be preferred for the introduction of pharmaceutically acceptable formulations of the viral vectors disclosed herein. The formation and use of liposomes is generally known to those of skill in the art (see for example, Couvreur *et al.*, 1977; Couvreur, 1988; Lasic, 1998; which describes the use of liposomes and nanocapsules in the targeted antibiotic therapy for intracellular bacterial infections and diseases). Recently, liposomes were developed with improved serum stability and circulation half-lives (Gabizon and Papahadjopoulos, 1988; Allen and Choun, 1987; U. S. Patent 5,741,516, specifically incorporated herein by reference in its entirety). Further, various methods of liposome and liposome like preparations as potential drug carriers have been reviewed (Takakura, 1998; Chandran *et al.*, 1997; Margalit, 1995; U. S. Patent 5,567,434; U. S. Patent 5,552,157; U. S. Patent 5,565,213; U. S. Patent 5,738,868 and U. S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, 1990; Muller *et al.*, 1990). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs (Heath and Martin, 1986; Heath *et al.*, 1986; Balazsovits *et al.*, 1989; Fresta and Puglisi, 1996), radiotherapeutic agents (Pikul *et al.*, 1987), enzymes (Imaizumi *et al.*, 1990a; Imaizumi *et al.*, 1990b), viruses (Faller and Baltimore, 1984), transcription factors and allosteric effectors (Nicolau and Gersonde, 1979) into a variety of cultured cell lines and animals. In addition, several successful clinical trails examining the effectiveness of liposome-mediated drug delivery have been completed (Lopez-Berestein *et al.*, 1985a; 1985b; Coune, 1988; Sculier *et al.*, 1988). Furthermore, several studies suggest that the use of liposomes is not associated with

autoimmune responses, toxicity or gonadal localization after systemic delivery (Mori and Fukatsu, 1992).

Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs). MLVs generally have diameters of from 25 nm to 4 μm. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 Å, containing an aqueous solution in the core.

Liposomes bear resemblance to cellular membranes and are contemplated for use in connection with the present invention as carriers for the peptide compositions. They are widely suitable as both water- and lipid-soluble substances can be entrapped, *i.e.* in the aqueous spaces and within the bilayer itself, respectively. It is possible that the drug-bearing liposomes may even be employed for site-specific delivery of active agents by selectively modifying the liposomal formulation.

In addition to the teachings of Couvreur *et al.* (1977; 1988), the following information may be utilized in generating liposomal formulations. Phospholipids can form a variety of structures other than liposomes when dispersed in water, depending on the molar ratio of lipid to water. At low ratios the liposome is the preferred structure. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations. Liposomes can show low permeability to ionic and polar substances, but at elevated temperatures undergo a phase transition which markedly alters their permeability. The phase transition involves a change from a closely packed, ordered structure, known as the gel state, to a loosely packed, less-ordered structure, known as the fluid state. This occurs at a characteristic phase-transition temperature, and results in an increase in permeability to ions, sugars, and drugs.

In addition to temperature, exposure to proteins can alter the permeability of liposomes. Certain soluble proteins such as cytochrome c bind, deform, and penetrate the bilayer, thereby causing changes in permeability. Cholesterol inhibits this penetration of proteins, apparently by packing the phospholipids more tightly. It is

contemplated that the most useful liposome formations for antibiotic and inhibitor delivery will contain cholesterol.

The ability to trap solutes varies between different types of liposomes. For example, MLVs are moderately efficient at trapping solutes, but SUVs are extremely inefficient. SUVs offer the advantage of homogeneity and reproducibility in size distribution, however, and a compromise between size and trapping efficiency is offered by large unilamellar vesicles (LUVs). These are prepared by ether evaporation and are three to four times more efficient at solute entrapment than MLVs.

In addition to liposome characteristics, an important determinant in entrapping compounds is the physicochemical properties of the compound itself. Polar compounds are trapped in the aqueous spaces and nonpolar compounds bind to the lipid bilayer of the vesicle. Polar compounds are released through permeation or when the bilayer is broken, but nonpolar compounds remain affiliated with the bilayer unless it is disrupted by temperature or exposure to lipoproteins. Both types show maximum efflux rates at the phase transition temperature.

Liposomes interact with cells *via* four different mechanisms: Endocytosis by phagocytic cells of the reticuloendothelial system such as macrophages and neutrophils; adsorption to the cell surface, either by nonspecific weak hydrophobic or electrostatic forces, or by specific interactions with cell-surface components; fusion with the plasma cell membrane by insertion of the lipid bilayer of the liposome into the plasma membrane, with simultaneous release of liposomal contents into the cytoplasm; and by transfer of liposomal lipids to cellular or subcellular membranes, or vice versa, without any association of the liposome contents. It often is difficult to determine which mechanism is operative and more than one may operate at the same time.

The fate and disposition of intravenously injected liposomes depend on their physical properties, such as size, fluidity and surface charge. They may persist in tissues for h or days, depending on their composition, and half lives in the blood range from min to several h. Larger liposomes, such as MLVs and LUVs, are taken up

rapidly by phagocytic cells of the reticuloendothelial system, but physiology of the circulatory system restrains the exit of such large species at most sites. They can exit only in places where large openings or pores exist in the capillary endothelium, such as the sinusoids of the liver or spleen. Thus, these organs are the predominate site of uptake. On the other hand, SUVs show a broader tissue distribution but still are sequestered highly in the liver and spleen. In general, this *in vivo* behavior limits the potential targeting of liposomes to only those organs and tissues accessible to their large size. These include the blood, liver, spleen, bone marrow and lymphoid organs.

Targeting is generally not a limitation in terms of the present invention. However, should specific targeting be desired, methods are available for this to be accomplished. Antibodies may be used to bind to the liposome surface and to direct the antibody and its drug contents to specific antigenic receptors located on a particular cell-type surface. Carbohydrate determinants (glycoprotein or glycolipid cell-surface components that play a role in cell-cell recognition, interaction and adhesion) may also be used as recognition sites as they have potential in directing liposomes to particular cell types. Mostly, it is contemplated that intravenous injection of liposomal preparations would be used, but other routes of administration are also conceivable.

Alternatively, the invention provides for pharmaceutically acceptable nanocapsule formulations of the polynucleotide compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (Henry-Michelland *et al.*, 1987; Quintanar-Guerrero *et al.*, 1998; Douglas *et al.*, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) should be designed using polymers able to be degraded *in vivo*. Biodegradable polyalkyl-cyanoacrylate nanoparticles that meet these requirements are contemplated for use in the present invention, and such particles may be are easily made, as described (Couvreur *et al.*, 1980; 1988; zur Muhlen *et al.*, 1998; Zambaux *et al.* 1998; Pinto-Alphandry *et al.*, 1995 and U. S. Patent 5,145,684, specifically incorporated herein by reference in its entirety

4.7 PHARMACEUTICAL COMPOSITIONS AND ROUTES OF ADMINISTRATION

In aspects of the invention involving administration of the vector compositions to an animal (*e.g.*, in gene therapy of a human subject), the vector compositions are preferably dispersed in a pharmaceutically acceptable excipient or solution. The pharmaceutical compositions comprising the vector compositions may be administered parenterally, intraperitoneally or topically. Solutions of the active compounds as a free base or a pharmacologically acceptable salt may also be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with several of the other

ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

For ophthalmic delivery regimens, the vector compositions may also be advantageously administered extraocularly or intraocularly, by topical application, inserts, injection, implants, or by cell therapy or gene therapy. For example, slow-releasing implants containing the vector compositions embedded in a biodegradable polymer matrix can deliver the vector compositions intra ocularly. The vector compositions may also be administered extracerebrally in a form that has been modified chemically or packaged so that it passes the blood-brain barrier, or it may be administered in connection with one or more agents capable of promoting penetration of the vector compositions across the barrier. Similarly, the vector compositions may be administered intraocularly, or may be administered extraocularly in connection with one or more agents capable of promoting penetration or transport of the vector compositions across the membranes of the eye.

As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The phrase "pharmaceutically acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. The preparation of an aqueous composition that contains a

protein as an active ingredient is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified.

The composition can be formulated in a neutral or salt form. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug release capsules and the like.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, sterile aqueous media that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage could be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, general safety and purity standards as required by FDA Office of Biologics standards.

4.8 THERAPEUTIC KITS

Additional embodiments of the present invention concern therapeutic kits that comprise, in a suitable container means, at least a first, or at least a first and a second rAAV vector in a pharmaceutically acceptable formulation. The vector compositions may comprise one or more polynucleotide sequences that encode all, or portions of one or more genes targeted for delivery to a selected host cell by the rAAV vector. These genes may encode full-length proteins, truncated proteins, site-specifically mutated proteins, or peptide epitopes. In other embodiments, the rAAV vector may comprise nucleic acid segments that encode enhancers, transcription factors, structural or regulatory proteins, ribozymes, or fusion proteins, and the like. Such nucleic acid segments may be either native, recombinant, or mutagenized nucleic acid segments. Kits comprising at least a first rAAV construct and instructions for using the construct (*e.g.*, in embodiments concerning gene therapy regimens) are also within the scope of the present invention. Such instructions may comprise information regarding the formulation, administration, dosage, or assay of the appropriate gene therapy constructs.

The kits may comprise a single container that may, if desired, contain a pharmaceutically acceptable sterile excipient, having associated with it the vector compositions. The single container means may contain a dry, or lyophilized, mixture of the viral vector composition, which may or may not require pre-wetting before use.

Alternatively, the kits of the invention may comprise a distinct container for each component. In such cases, separate or distinct containers would contain the viral vector, either as a sterile DNA solution or in a lyophilized form. The kits may also comprise a third container for containing a sterile, pharmaceutically acceptable buffer, diluent or solvent. Such a solution may be required to formulate the vector components into a more suitable form for application to the body, *e.g.*, as an intravenous or other injectable form(s). It should be noted, however, that all components of a kit could be supplied in a dry form (lyophilized), which would allow for "wetting" upon contact with body fluids. Thus, the presence of any type of

pharmaceutically acceptable buffer or solvent is not a requirement for the kits of the invention.

The container(s) will generally be a container such as a vial, test tube, flask, bottle, syringe or other container, into which the components of the kit may placed. The compositions may also be aliquoted into smaller containers, should this be desired. The kits of the present invention may also include material for containing the individual containers in close confinement for commercial sale, such as, *e.g.*, injection or blow-molded plastic containers into which the desired vials or syringes are retained. Irrespective of the number of containers, the kits of the invention may also comprise, or be packaged with, an instrument for assisting with the placement of the vector compositions within the body of an animal. Such an instrument may be a syringe, pipette, forceps, or any such medically approved delivery vehicle. Likewise, the kit may also comprise one or more sets of instructions for use of the kit, for delivery of the vector to a selected host cell, or for storage and handling of the kit and its contents.

4.9 Kits for Large-Scale Preparation of rAAV or HSV Vectors

Additional embodiments of the present invention concern kits that comprise, in a suitable container means, at least a first DNA segment comprising an AAV *rep* coding sequence operably linked to a promoter, an AAV *cap* coding sequence operably linked to a promoter, an HSV-1 origin of replication and an HSV-1 packaging sequence. Such kits may also comprise an HSV-1 helper virus.

The kits may comprise a single container that contains the DNA segment and the helper virus, or the DNA segment and helper virus may be contained in distinct containers. Kits that comprise a recombinant herpes simplex virus vector comprising an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter are also provided.

Such kits may also include material for containing the individual containers in close confinement for commercial sale, such as, *e.g.*, injection or blow-molded plastic containers into which the desired vials or syringes are retained. Irrespective of the

number of containers, the kits of the invention may also comprise one or more sets of instructions for use of the kit, for delivery of the vector to a selected host cell, or for storage and handling of the kit and its contents. Such instructions may provide protocols for the large-scale preparation of the vector components, and may include such information as growth conditions, isolation and purification methodologies, and other parameters for preparation of the final vector compositions

4.10 Nucleic Acid Amplification and Site-Specific Mutagenesis

Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent polypeptides, through specific mutagenesis of the underlying polynucleotides that encode them. The technique, well-known to those of skill in the art, further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter the activity or effectiveness of such viral vector constructs in a transformed host cell. Likewise in certain embodiments, the inventors contemplate the mutagenesis of the viral genome itself to facilitate improved infectivity, replication, stability, activity, or viral titers, as well as efficiency of transfection both *in vitro* and/or *in vivo*.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands f a

double-stranded vector which includes within its sequence a DNA sequence which encodes the desired polypeptide(s). An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected polynucleotide segments using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting, as there are other ways in which sequence variants of polypeptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding a desired polypeptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation that result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a

DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent 4,237,224, specifically incorporated herein by reference in its entirety. Nucleic acids, used as a template for amplification methods, may be isolated from cells according to standard methodologies (Sambrook *et al.*, 1989). The nucleic acid may be genomic DNA or fractionated or whole cell RNA. Where RNA is used, it may be desired to convert the RNA to a complementary DNA. In one embodiment, the RNA is whole cell RNA and is used directly as the template for amplification.

Pairs of primers that selectively hybridize to nucleic acids corresponding to the ribozymes or conserved flanking regions are contacted with the isolated nucleic acid under conditions that permit selective hybridization. The term "primer," as defined herein, is meant to encompass any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent process. Typically, primers are oligonucleotides from ten to twenty base pairs in length, but longer sequences can be employed. Primers may be provided in double-stranded or single-stranded form, although the single-stranded form is preferred.

Once hybridized, the nucleic acid:primer complex is contacted with one or more enzymes that facilitate template-dependent nucleic acid synthesis. Multiple rounds of amplification, also referred to as "cycles," are conducted until a sufficient amount of amplification product is produced.

Next, the amplification product is detected. In certain applications, the detection may be performed by visual means. Alternatively, the detection may involve indirect identification of the product *via* chemiluminescence, radioactive scintigraphy of incorporated radiolabel or fluorescent label or even *via* a system using electrical or thermal impulse signals (Affymax technology).

A number of template dependent processes are available to amplify the marker sequences present in a given template sample. One of the best-known amplification methods is the polymerase chain reaction (referred to as PCR™) which is described in detail in U. S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, and each incorporated herein by reference in entirety.

Briefly, in PCR™, two primer sequences are prepared that are complementary to regions on opposite complementary strands of the marker sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase, *e.g.*, *Taq* polymerase. If the marker sequence is present in a sample, the primers will bind to the marker and the polymerase will cause the primers to be extended along the marker sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the marker to form reaction products, excess primers will bind to the marker and to the reaction products and the process is repeated.

A reverse transcriptase PCR amplification procedure may be performed in order to quantify the amount of mRNA amplified. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook *et al.*, 1989. Alternative methods for reverse transcription utilize thermostable, RNA-dependent DNA polymerases. These methods are described in WO 90/07641, filed December 21, 1990, incorporated herein by reference. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction ("LCR"), disclosed in Eur. Pat. Appl. No. 320308, incorporated herein by reference in its entirety. In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCR, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U. S. Patent 4,883,750 describes a method similar to LCR for binding probe pairs to a target sequence.

Qbeta Replicase (QβR), described in Intl. Pat. Appl. Publ. No. PCT/US87/00880, incorporated herein by reference, may also be used as still another amplification method in the present invention. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a sample in the

presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain nucleotide 5'-[alpha-thio]-triphosphates in one strand of a restriction site may also be useful in the amplification of nucleic acids in the present invention.

Strand Displacement Amplification (SDA), described in U. S. Patent Nos. 5,455,166, 5,648,211, 5,712,124 and 5,744,311, each incorporated herein by reference, is another method of carrying out isothermal amplification of nucleic acids which involves multiple rounds of strand displacement and synthesis, *i.e.*, nick translation. A similar method, called Repair Chain Reaction (RCR), involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as biotinylated derivatives for easy detection. A similar approach is used in SDA. Target specific sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having 3' and 5' sequences of non-specific DNA and a middle sequence of specific RNA is hybridized to DNA that is present in a sample. Upon hybridization, the reaction is treated with RNase H, and the products of the probe identified as distinctive products that are released after digestion. The original template is annealed to another cycling probe and the reaction is repeated.

Still another amplification methods described in Great Britain Patent 2202328, and in Intl. Pat. Appl. Publ. No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety, may be used in accordance with the present invention. In the former application, "modified" primers are used in a PCR-like, template- and enzyme-dependent synthesis. The primers may be modified by labeling with a capture moiety (*e.g.*, biotin) and/or a detector moiety (*e.g.*, enzyme). In the latter application, an excess of labeled probes is added to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the target sequence is released intact, available to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS), including nucleic acid sequence based amplification (NASBA) and 3SR Gingeras *et al.*, PCT Application WO 88/10315, incorporated herein by reference. In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction, heat denaturation of a clinical sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer that has target specific sequences. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target specific primer, followed by polymerization. The double-stranded DNA molecules are then multiply transcribed by an RNA polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNA's are reverse transcribed into single stranded DNA, which is then converted to double-stranded DNA, and then transcribed once again with an RNA polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target specific sequences.

Davey *et al.*, Eur. Pat. Appl. No. 329822 (incorporated herein by reference in its entirety) disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from the resulting DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in duplex with either DNA or RNA). The resultant ssDNA is a template for a second primer, which also includes the sequences of an RNA polymerase promoter (exemplified by T7 RNA polymerase) 5' to its homology to the template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" fragment of *E. coli* DNA polymerase I), resulting in a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA

between the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification. With proper choice of enzymes, this amplification can be done isothermally without addition of enzymes at each cycle. Because of the cyclical nature of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

Miller *et al.*, PCT Application WO 89/06700 (incorporated herein by reference in its entirety) disclose a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic, *i.e.*, new templates are not produced from the resultant RNA transcripts. Other amplification methods include "RACE" and "one-sided PCR" (Frohman, 1990 incorporated by reference).

Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, may also be used in the amplification step of the present invention.

Following any amplification, it may be desirable to separate the amplification product from the template and the excess primer for the purpose of determining whether specific amplification has occurred. In one embodiment, amplification products are separated by agarose, agarose-acrylamide or polyacrylamide gel electrophoresis using standard methods (Sambrook *et al.*, 1989).

Alternatively, chromatographic techniques may be employed to effect separation. There are many kinds of chromatography which may be used in the present invention: adsorption, partition, ion exchange and molecular sieve, and many specialized techniques for using them including column, paper, thin-layer and gas chromatography.

Amplification products must be visualized in order to confirm amplification of the marker sequences. One typical visualization method involves staining of a gel

with ethidium bromide and visualization under UV light. Alternatively, if the amplification products are integrally labeled with radio- or fluorometrically-labeled nucleotides, the amplification products can then be exposed to x-ray film or visualized under the appropriate stimulating spectra, following separation.

In one embodiment, visualization is achieved indirectly. Following separation of amplification products, a labeled, nucleic acid probe is brought into contact with the amplified marker sequence. The probe preferably is conjugated to a chromophore but may be radiolabeled. In another embodiment, the probe is conjugated to a binding partner, such as an antibody or biotin, and the other member of the binding pair carries a detectable moiety.

In one embodiment, detection is by Southern blotting and hybridization with a labeled probe. The techniques involved in Southern blotting are well known to those of skill in the art and can be found in many standard books on molecular protocols (Sambrook *et al.*, 1989). Briefly, amplification products are separated by gel electrophoresis. The gel is then contacted with a membrane, such as nitrocellulose, permitting transfer of the nucleic acid and non-covalent binding. Subsequently, the membrane is incubated with a chromophore-conjugated probe that is capable of hybridizing with a target amplification product. Detection is by exposure of the membrane to x-ray film or ion-emitting detection devices.

One example of the foregoing is described in U. S. Patent 5,279,721, incorporated by reference herein, which discloses an apparatus and method for the automated electrophoresis and transfer of nucleic acids. The apparatus permits electrophoresis and blotting without external manipulation of the gel and is ideally suited to carrying out methods according to the present invention.

4.11 BIOLOGICAL FUNCTIONAL EQUIVALENTS

Modification and changes may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that still possesses desirable characteristics. As mentioned above, it is often desirable to introduce one or more mutations into a specific polynucleotide sequence. In certain

circumstances, the resulting encoded polypeptide sequence is altered by this mutation, or in other cases, the sequence of the polypeptide is unchanged by one or more mutations in the encoding polynucleotide.

When it is desirable to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, second-generation molecule, the amino acid changes may be achieved by changing one or more of the codons of the encoding DNA sequence, according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the polynucleotide sequences disclosed herein, without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporate herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of

their hydrophobicity and charge characteristics (Kyte and Doolittle, 1982), these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (–0.4); threonine (–0.7); serine (-0.8); tryptophan (–0.9); tyrosine (–1.3); proline (–1.6); histidine (–3.2); glutamate (-3.5); glutamine (–3.5); aspartate (–3.5); asparagine (–3.5); lysine (–3.9); and arginine (–4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those that are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (–0.4); proline (–0.5 ± 1); alanine (–0.5); histidine (–0.5); cysteine (-1.0); methionine (–1.3); valine (–1.5); leucine (–1.8); isoleucine (–1.8); tyrosine (-2.3); phenylalanine (–2.5); tryptophan (–3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those that are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their

hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions which take several of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

5.0 EXAMPLES

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventors to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

5.1 EXAMPLE 1 - MATERIALS AND METHODS

Abbreviations used include: AAV, Adeno-associated virus; Ad, Adenovirus; HSV-1, Herpes simplex virus-1; MOI, multiplicity of infection; pfu, plaque-forming units; wt, wild type.

5.1.1 CELL LINES

HeLa cells were maintained in Dulbecco's modified Eagle's media (DMEM, Gibco-BRL, Grand Island, NY) that contained 10% heat inactivated fetal calf serum (FCS). Vero cells were maintained in DMEM which contained 5% FCS. The V27 cell line, a neomycin resistant Vero cell line capable of expressing ICP27, was maintained in DMEM which contained 10% FCS and has already been described (Rice and Knipe, 1990). All 293 cell lines were maintained in DMEM which contained 10% FCS. Cells were cultured at 37°C in 5% CO_2.

The UF2-293 cell line was generated by transfection of a 10 cm dish of 293 cells (from ATCC) with 10 μg of pUF2 DNA (Zolotukhin *et al.*, 1996). The cells

were then passaged in 600 μg/ml G418 (Gibco-BRL) for three weeks. Surviving cells were then sorted using fluorescence-activated cell sorting (FACS), utilizing the adsorption and emission spectrum of the humanized green fluorescent protein (hGFP) to isolate high expressing cells (Zolotukhin *et al.*, 1996). Cells were considered high expressors when on adsorption of light of 395 nm wavelength, emitted light of 509 nm wavelength at an intensity 125 times greater than the emission of similarly stimulated, non-transfected 293 cells. The high expressors were maintained in G418 at 600 μg/ml.

The GFP-92 cell line was created by infecting 293 cells with rAAV-UF2. Cells were passaged in 200 μg G418 for two weeks and screened for GFP fluorescence. Colonies were isolated and analyzed by PCR™, as described below, for their ability to produce rAAV when transfected with pIM45 DNA and superinfected with adenovirus (Ad5). A producer cell line was identified and single clones were again isolated and analyzed for their ability to produce rAAV.

5.1.2 PLASMIDS

The plasmids pUF2, psub201, pIM45 and pRS5 have been previously described (Flotte *et al.*, 1995; Pereira *et al.*, 1997; Samulski *et al.*, 1987; Zolotukhin *et al.*, 1996). pUF2 is a bicistronic vector containing the human cytomegalovirus (HCMV) major immediate early (MIE) enhancer driving humanized green fluorescent protein (*hgfp*) and the HSV-1 thymidine kinase promoter driving a neomycin resistant gene inserted between AAV-2 ITRs. pRS5 and pIM45 are helper plasmids that supply Rep and Cap for generating rAAV. pAAV2 is a pKS based vector containing the AAV-2 genome. pAAV-*lacZ* is a HCMV MIE driven *lacZ* reporter construct inserted between AAV-2 ITRs.

pHSV-RC was used to generate the HSV-1 amplicons HSV-RC/KOS and HSV-RC/d27 and is a pUC19-derived vector (FIG. 1). The *a*-sequence contains the HSV-1 packaging signals and was cloned into the *Eco*RI site of pUC19. The *oriS* sequence contains an HSV-1 origin of replication (the internal *Sma*I fragment from the HSV-1 *ori S)* and was inserted at *Sma*I to generate pHSV. To create pHSV-RC,

the *rep* and *cap* genes from AAV-2 were isolated from psub201 by an *Xba*I digest and cloned onto the *Xba*I site of pHSV (FIG. 1).

pHSV-gfp was constructed from pHSV and p1.1-gfp (a vector expressing the green fluorescent protein (GFP). p1.1-gfp was *Not*I digested and Klenow blunted. This fragment was then cloned into the *Sph*I digested and T4 polymerase blunted pHSV to create pHSV-gfp. p43-hgfp is based on the pUF2 vector. The expression cassette from pCI (isolated by a *BamH*I - *Bgl*II digest) was cloned between the ITRs of *Bgl*II digested pUF2 to create p43. The *hgfp* cDNA was isolated from pUF2 by a *Not*I digest and then cloned into the *Not*I site of the p43 to create p43-hgfp. pCI-hgfp was created by cloning *hgfp* into the *Not*I site of pCI. The 115 base pair deletion vector pCI-hgfpd was created by *PflM*I and *Pvu*II digestion of pCI-hgfp, followed by T4 polymerase blunting of the overhanging ends, and then self-ligation of the vector.

5.1.3 TRANSFECTION

Transfections for the rescue of rAAV genomes from pAAV-*lacZ* were performed using Lipofectamine (Gibco-BRL), following the manufacturer's protocol 24 h after seeding 2×10^5 HeLa cells onto 6 well plates. The UF2-293 cell line was generated by plating 1×10^6 293 cells onto a 10-cm dish followed by transfection with 10 μg of pUF2. This transfection was done by precipitation of plasmid DNA with $CaCl_2$ in 2× N,N-bis(2-hydroxyethyl)-2-aminoethane-sulfonic acid (BES), (25mM, pH 6.95). The transfected cells were incubated at 35°C, 3% CO_2 overnight. The transfected cells were rinsed once with phosphate buffered saline (PBS, pH 7.4) and grown in DMEM with 10% FCS. The GFP-92 cell line was created by seeding 1×10^6 293 cells on a 10 cm plate followed by transfection with 10 μg of pUF2 DNA by $CaCl_2$ coprecipitation in HEPES buffered saline. To generate the first passage of the amplicons HSV-RC/KOS and HSV-GFP/KOS, 1×10^6 Vero cells were plated onto 10 cm dishes followed by transfection with 10 μg of pHSV-RC and 10 μg of HSV-1 (KOS) DNA or 10 μg of pHSV-gfp and 10 μg of HSV-1 (KOS) DNA by BES coprecipitation. To generate the first passage HSV-RC/d27, 1×10^6 V27 cells were plated onto 10 cm dishes and transfected 24 h later with 20 μg of pHSV-RC DNA

using Lipofectamine. To produce rAAVUF2 from the GFP-92 cells by transfection, 2×10^6 cells were plated onto a 10 cm dish and transfected with 8 μg of pRS5 DNA using Lipofectamine.

5.1.4 VIRUS

HSV-1 (wt KOS strain) was propagated by infecting Vero cells (90% confluent in T175 flasks) at a multiplicity of infection (MOI) of 0.1 per cell. Adsorption of virus was done for 45 min in reduced serum DMEM (2% FCS). After full cytopathic effect (CPE) was observed (usually 48 h post infection) the cell pellet was collected by centrifugation (1000 rpm for 10 min), then frozen and thawed 3 times. Cell debris was removed by centrifugation (3000 rpm for 5 min). d27-1 is an ICP27 deletion of HSV-1 (KOS strain) and has been previously described (Rice and Knipe, 1990). d27-1 was propagated as described for HSV-1 except that the complementing cell line, V27, was used. Ad5 (from the American *Type Culture* Collection, Rockville, MD) was propagated by infecting 293 cells (90% confluent in 15 cm dishes) at an MOI of 0.1 per cell. Ad5 was harvested as described for HSV-1 after full CPE was observed (usually 72 to 96 h post infection). AAV-2 was propagated by coinfection of 293 cells with AAV-2 (MOI of 200 particles per cell) and Ad5 (MOI of 0.1). AAV-2 viral lysates were prepared by freeze-thaw, and the Ad5 was heat inactivated by incubation at 55°C for 45 min. HSV-1 (wt KOS) was titered by plaque forming assay on Vero cells. d27-1 was titered by plaque forming assay on V27 cells. Analysis of d27-1 stocks for the presence of wt HSV-1 was done by plaque assay on non-complementing Vero cells (< 100 pfu/ml detected). Ad5 was titered by plaque forming assay on 293 cells. AAV-2 was titered for particles by dot blot analysis as described below for recombinant genomes in the amplicon stocks.

HSV-RC/KOS was propagated by harvesting the cell pellet by centrifugation (1000 rpm for 10 min) after full CPE was observed in the transfected cells. The cell pellet was frozen and thawed three times and cell debris removed by centrifugation (3000 rpm for 5 min). One fourth of the virus was then used to infect Vero cells (90% confluent in T175 flasks) as previously described to generate the second passage of

HSV-RC/KOS. One fourth of the virus was used to infect Vero cells in T175 flasks to generate each successive passage. HSV-RC/d27 was generated by superinfection of the pHSV-RC transfected V27 cells with d27-1 virus 36 h post transfection at an MOI of 2.5. The cell pellet was collected as previously described after full CPE was observed (72 h post infection). Successive passages of HSV-RC/d27 were generated as described for HSV-RC/KOS except that the complementing cell line, V27, was used. Fourth passage or greater amplicon stocks were used in the studies described.

Each amplicon stock was titered for the presence of helper virus by a plaque-forming assay on the appropriate cell line (Vero cells for HSV-RC/KOS, V27 cells for HSV-RC/d27). The titers of HSV-1 in HSV-RC/KOS, in passages 2 through 6, varied between 1×10^8 and 3×10^8. The titer of d27-1 in HSV-RC/d27, in passage 2 through 5, varied between 1×10^7 and 3×10^7 pfu/ml. HSV-RC/d27 was analyzed for the presence of wt HSV-1 by plaque assay on non-complementing Vero cells (< 100 pfu/ml detected). The titer of recombinant genomes (the *rep* and *cap* genome from pHSV-RC) in each amplicon stock was determined by dot blot analysis of the stocks. Aliquots of the virus were DNAseI treated for 2 h at 37°C in DNAseI buffer (final concentration 10mM Tris (pH 7.4), 10mM KCl, 1.5mM $MgCl_2$) and then proteinase K treated for 2 h at 55°C in proteinase K buffer (final concentration 10 mM Tris (pH 7.4), 5mM EDTA, 0.5% SDS). 5 µl of 5N NaOH was then added to the samples and they were incubated at 65°C for 1 h. The samples were neutralized with 50 µl of 2N NH_4OH and were then transferred using a vacuum apparatus to a nylon membrane that was first equilibrated with 1N NH_4OH for 1 h. The slots were then washed with 50 µl of 2N NH_4OH. A standard curve of serial dilutions of HSV-1 was processed and applied to the membrane in an identical fashion.

A standard curve of serial dilutions of pHSV-RC was denatured, neutralized and also applied to the membrane. The membrane was then incubated with prehybridization solution (1% SDS, 5 mg/ml nonfat dried milk, 0.05 mg/ml heparin, 0.2 mg/ml denatured salmon sperm DNA, 60 mg/ml PEG 8000, 5× SSPE (750 mM NaCl, 50 mM Na_2HPO_4, 5 mM EDTA, and 10% formamide) for 4 h at 60°C. The membrane was hybridized overnight at 60°C in the prehybridization solution with

[α-^{32}P] dATP labeled, random primer generated probe. The probe was generated from a 2.1 kb *cap* fragment isolated by *KpnI* digestion of psub201. After hybridization, the membrane was then washed twice in 0.1× SSC and 0.1% SDS at 65°C for 45 min. The membrane was exposed to film for 24-48 h at -70°C. The titer of recombinant genomes varied between 3×10^7 to 7×10^7 recombinant genomes per ml for HSV-RC/KOS and 1×10^7 to 3×10^7 recombinant genomes per ml for HSV-RC/d27. The specificity of the probe for recombinant genomes and not HSV-1 genomes was confirmed by demonstrating that the HSV-1 standard curve did not produce a signal when the membrane was hybridized with probe for the recombinant genomes. To verify that the HSV-1 DNA did transfer, the membrane was stripped by washing the membrane with 0.1× SSC and 0.1% SDS at 100°C and then rehybridized with an [α-^{32}P] dATP labeled *oriS* DNA probe. The membranes were then processed as described above.

The packaging, purification and titering of rAAVlacZ has been described previously (Kessler *et al.*, 1996). rAAVUF2 was prepared from six T175 flasks of UF2-293 cells. Flasks were infected with HSV-RC/KOS (MOI of the HSV-RC/KOS was 2 recombinant genomes per cell and 2.5 pfu of HSV-1 per cell) when the cells were 90% confluent (10^8 cells). The total number of cells in the preparation was determined by counting the number of cells present on a similarly prepared flask using a hemocytometer. 48 h later (after full CPE), the cells were centrifuged for 10 min at 1000 rpm. The cell pellet was then frozen and thawed three times and cell debris was removed by centrifugation at 3000 rpm for 10 min. The sample was heat inactivated for 1 h at 55°C and DNAseI treated for 1 h at 37°C in DNAse buffer. Virus was purified on an isopycnic CsCl gradient as described (Kessler *et al.*, 1996). 100 µl fractions were collected, the refractive index was determined for each fraction, and each fraction was then analyzed for the presence of rAAVUF2 by infecting HeLa cells in the presence of Ad5 and directly observing the cells by fluorescent microscopy for the presence of hGFP expression 36 h later. 2×10^5 HeLa cells were plated onto 6 well dishes 24 h before coinfection with 1 µl of each CsCl fraction and Ad5 (MOI of 2). Positive fractions were pooled and dialyzed overnight against 4 l of

10 mM Tris, 1 mM EDTA (pH 7.4). The presence of infectious rAAVUF2 was determined by replication assay as described below. No contaminating HSV-1 was detected in a Vero cell plaque assay with a sensitivity of detection greater than 100 pfu/ml.

rAAVUF2 was prepared from GFP-92 cells by one of three methods. Thirty 10 cm plates were seeded with 2×10^6 cells, and 24 h later the cells were either transfected with pRS5 as described above or infected with HSV-RC/d27 (MOI of the HSV-RC/d27 was one recombinant genome per cell and one pfu of d27-1 per cell). The total cell number in each preparation was determined by counting the cells on identically seeded plates using a hemocytometer. For the transfection method, the transfection solution was removed 8 h later and Ad5 (MOI of 2.5) was added to the cells in DMEM with 10% FCS. One group of plates that was infected with HSV-RC/d27 was superinfected with wt HSV-1 (MOI of 1) 12 h later. The cells were collected after full CPE had developed and processed as described above.

5.1.5 Replication Assays

Rescue and replication of rAAV genomes from transfected plasmids, producer cell lines or infected rAAV particles was demonstrated by first seeding 2×10^5 HeLa cells onto 6 well plates or 1×10^6 HeLa cells onto 10 cm dishes. After 24 h, the cells were either mock transfected, mock infected, transfected with a rAAV plasmid, infected with AAV-2, infected with rAAV virus or a combination of these (as described in the brief description of the figures). After an additional 24 h, the cells were either mock infected, infected with HSV-1, infected with d27-1, or infected with one of the amplicons (as described in the brief description of the figures). Cells were harvested 36 h later and centrifuged for 5 min at 2000 rpm. Media was removed and small molecular weight DNA was isolated from the pellet by Hirt extraction (Hirt, 1967). 10 µg of Hirt extracted DNA was loaded per lane on a 0.8% agarose gel and run for 12 h at 25V. DNA from the gel was transferred to a nylon membrane by Southern blotting. The nylon membrane was then prehybridized and hybridized and as described above. The different templates used to generate the [α-^{32}P] dATP labeled

probes were a 3.3-kb *lacZ* DNA fragment, a 4.4-kb AAV-2 DNA fragment, and a 700-bp *hgfp* DNA fragment. The membranes were stripped as described above and reprobed for the presence of replicating wt AAV genomes using an [α-^{32}P] dATP-labeled 2.1-kb *cap* fragment (isolated by *Kpn*I digestion of psub201). For the *Dpn*I assay, 10 µg of Hirt extracted DNA was extensively digested with *Dpn*I (100U) for 24 h, ethanol precipitated and run on a 0.8% agarose gel for 12 h at 25V.

5.1.6 PCR™ ASSAYS

Samples from clarified cell lysates (70 µl from 7 ml for detection of rAAVUF2 made from the cell line UF2-293 with HSV-RC/KOS, 2 µl from 3 ml for detection of rAAVUF2 made from the GFP-92 cell line with HSV-RC/d27, 100 µl from 3 ml for wt AAV detection) were treated with 50U DNAseI for 2 h at 37°C in DNAseI buffer and then proteinase K digested in proteinase K buffer for 2 h at 55°C. The samples were then phenol and chloroform extracted and ethanol precipitated followed by centrifugation at 14,000 rpm for 30 min at 4°C to pellet the DNA. The DNA pellet was rinsed once with 70% ethanol, then dried, and reconstituted in dH_2O. An aliquot of this sample (1 µl from 20 µl for rAAVUF2 and 9 µl of 10 µl for wt AAV) was used in the PCR™ reactions. PCR™ reactions were carried out in a 50-µl volume, and PCR™ products (15 µl) were analyzed on 2% agarose gels at 100V. For the quantitative-competitive PCR™ (QC-PCR™), the products were analyzed on 2% agarose gels for 3 h at 50V. A Stratagene Eagle Eye™ detection system was used to record the images.

The primers used to detect rAAVUF2 particles anneal to the coding region of *hfgp* and generate a 700 bp product. The *hgfp* sense primer was 5'-ATGAGCAAGGGCGAGGAACTGTTC-3' (SEQ ID NO:1). The *hgfp* antisense primer was 5'-TCACTTGTACAGCTCGTCCATGCC-3' (SEQ ID NO:2). The positive control was 200 pg of p43-hgfp. The PCR™ conditions were: 4 min at 94°C; 25 cycles of 60 seconds at 94°C, 30 seconds at 60°C, 60 seconds at 72°C; and then 4 min at 72°C.

The primers used to detect the presence of wt AAV anneal to the ITR *D* sequence and to the *cap* coding sequence and generate a 370 bp product. The *D* sequence primer was 5'-CTCCATCACTAGGGGTTCC -3' (SEQ ID NO:3). The *cap* primer was 5'-CTTCATCACACAGTACTCCACGGG-3' (SEQ ID NO:4). The positive controls were serial dilutions of pAAV2. The PCR™ conditions were identical to those used with the *hgfp* primers except that 30 cycles were completed. Typically 10 fg of pAAV2 could be detected by PCR™ amplification after ethidium bromide staining.

A particle count of rAAVUF2 was determined by QC- PCR™ and was based on the determination of the amount of rAAVUF2 template present in a sample through comparison with a known quantity of internal control standard. The internal control for the QC-PCR™ reactions, pCI-hgfpd, was identical to the *hgfp* sequence to which the primers annealed and amplified except that an internal deletion was made as described above. The *hgfp* primers generate a 585 bp product when pCI-hgfpd is used as the template. A constant amount of rAAVUF2 DNA was added to each QC-PCR™ reaction (1 μl) and the amount of internal control was varied to produce a standard curve (see brief description of the figures for exact amounts of pCI-hgfpd added to each reaction). The amount of rAAVUF2 template present was then determined by identifying the amount of internal control DNA that had to be added which would give full size and deleted PCR™ products of equal intensity after ethidium bromide staining. The number of single strand template genomes present (the number of particles) was then calculated.

The PCR™ detection of rAAVUF2 particles does not give a false positive result under the conditions used. As a negative control for the specificity of the PCR™ analysis to detect actual rAAV particles and not residual DNA template from undigested cellular DNA, 1×10^8 GFP-92 cells were pelleted and reconstituted in 1ml of DMEM. The cells were then frozen and thawed three times. The cell debris was removed by centrifugation at 3000 rpm for 10 min and DMEM was added to the lysate so that the final volume was 1 ml. 100 μl of this sample was DNAseI and proteinase K treated, phenol and chloroform extracted, precipitated and reconstituted

in 20 µl dH_2O. 5 µl (out of 20 µl) of the negative control did not give a detectable PCR™ product when the *hgfp* primers and PCR™ conditions that were used for all *hgfp* PCR™ reactions were employed for thirty amplification cycles.

5.2 EXAMPLE 2 - CONSTRUCTION OF HSV-1 AMPLICON WHICH CONTAINS REP, AN HSV-1 ORIGIN OF REPLICATION AND HSV-1 PACKAGING

The expression of Rep 78 or 68 has been shown to inhibit the replication of DNA viruses. Rep interacts with Ad and cellular DNA replication in viral replication centers and disrupts their subsequent formation and function (Weitzman *et al.*, 1996a, 1996b). Expression of the Rep protein also inhibits HSV-1 induced cellular DNA amplification and HSV-1 viral DNA replication itself (Heilbronn *et al.*, 1990).

It was considered possible that the expression of Rep interfered with HSV-1 DNA replication to such an extent that creation of amplicon stocks of reasonable titer would not be possible. Similar problems were previously observed by multiple investigators attempting to create a recombinant Ad vector expressing Rep.

To determine if an amplicon system that expressed Rep could be created, a plasmid that expresses Rep from the p5 and p19 promoters was constructed, pHSV-RC (FIG. 1). When pHSV-RC was cotransfected with HSV-1 (KOS) DNA into Vero cells, it took 48 h longer for induction of full CPE than when HSV-1 DNA and pUC19 or when HSV-1 DNA and pHSV-gfp (a non-Rep expressing control amplicon plasmid) were transfected (7 days for full CPE *vs.* 5 days). In subsequent passages (P2-P6), no difference was seen in the time course of CPE for the different amplicon stocks (48 h for full CPE). Also, the titers of plaque forming HSV-1 and recombinant genomes in the different passages did not vary a great deal (HSV-1 titer varied from 1×10^8 to 3×10^8 pfu/ml, recombinant genome dot blot titer varied from 3×10^7 to 7×10^7 genomes/ml.

5.3 EXAMPLE 3 - RESCUE AND REPLICATION OF rAAV GENOMES IS SUPPORTED BY HSV-1 AMPLICON EXPRESSING REP FROM THE P5 AND P19 PROMOTERS AND MADE WITH HSV-1 HELPER VIRUS (HSV-RC/KOS)

The HSV-1 amplicon had to be able to rescue and replicate rAAV genomes efficiently if the HSV-1 amplicon system expressing Rep and Cap were to be successful at packaging rAAV genomes into virions. Rescue and replication of rAAV genomes by HSV-RC/KOS requires the appropriate expression of Rep from the p5 and p19 promoters, which are in a different genomic structural context than they are in the wt AAV genome. Additionally, expression of Rep from the amplicon genome has to be appropriately timed with HSV-1 early gene expression so that rAAV replication proceeds, as does wt AAV replication.

The ability of HSV-RC/KOS to replicate rAAV genomes introduced into cells by infection of rAAV virions, by transfection as plasmids, or when maintained as proviral rAAV genomes integrated into cellular chromosomal DNA was analyzed.

The ability of HSV-RC/KOS to replicate and amplify a rAAV genome (rAAV*lacZ*) after rAAV infection was examined. HeLa cells (2×10^5) were seeded onto 6 well plates. After 24 h, the cultures were either mock infected, infected with rAAV*lacZ* (5×10^4 particles), AAV-2 (MOI of 1000 particles per cell) or both. The cells were infected with HSV-1 (KOS strain, MOI of 2), or HSV-RC/KOS (MOI of the HSV-RC/KOS was one recombinant genome per cell and 2 pfu of HSV-1 per cell) 24 h later. The wells were scraped and the cells were collected and centrifuged (2000 rpm, 5 min) after 36 h. Media was removed and the small molecular weight DNA in the pellet was isolated by Hirt extraction. Hirt extracted DNA (5 μg) was loaded per lane on a 0.8% agarose gel and run for 12 h at 25V. DNA from the gel was transferred to Nylon membrane by Southern blotting, and probed with an [α-^{32}P] dATP-labeled *lacZ* DNA probe or an [α-^{32}P] dATP-labeled psub201 DNA probe.

In this assay, replicative intermediates of rAAV, the double stranded monomers (RF_m), double stranded dimers (RF_d), and higher molecular weight replicative forms, indicate successful replication. Positive replication was observed in

samples in which small molecular weight DNA was analyzed from cells coinfected with rAAV, AAV-2 and HSV-1 (positive control) or coinfected with rAAV and HSV-RC/KOS. Replicative forms of rAAV were not detectable in any of the other samples.

These data illustrate that HSV-1 gene expression and Rep expression from an HSV-1 amplicon is temporally and quantitatively appropriate for the task of replicating rAAV genomes introduced into cells by viral infection. In addition, the intensity of the RF_m and RF_d in cells coinfected with rAAV and HSV-RC/KOS, as compared to cells coinfected with rAAV, AAV-2 and HSV-1, suggests that Rep expression from an amplicon in the presence of HSV-1 coinfection is capable of supporting rAAV replication at a higher level than AAV-2 and HSV-1 at similar multiplicities of infection. This may be due to the absence of replication competent AAV-2 in HSV-RC/KOS. Replication competent AAV-2 would successfully compete with rAAV for replication machinery and lead to a decrease in rAAV replication (Clark *et al.*, 1996).

These results also demonstrate that wt AAV is not generated and amplified by an HSV-1 amplicon expressing Rep protein. The RF_m and RF_d of wt AAV were only observed in the samples in which Hirt extracted DNA was analyzed from cells coinfected with AAV-2 and HSV-1 and probed for *rep* and *cap* sequences. In addition, a 7-day exposure of the Southern blot did not reveal any replicative forms of wt AAV in any additional samples. Normally, replication of wt AAV replicative forms is observable after 48 h exposure of the Southern blot.

The ability of HSV-RC/KOS to rescue and replicate rAAV genomes from different rAAV templates was also evaluated. These data indicate that HSV-RC/KOS was able to rescue and replicate rAAV genomes from transfected plasmids. HeLa cells were seeded onto 6 well plates (2×10^5). The cells were either mock transfected, transfected with 3 μg of pAAV*lacZ*, or infected with rAAVlacZ (5×10^4 particles) 24 hours later. The plasmid pAAV*lacZ* contains a HCMV MIE driven *lacZ* expression cassette flanked by ITRs. The cells were either mock infected, infected with wt HSV-1 (MOI of 2) or infected with HSV-RC/KOS (MOI of the

HSV-RC/KOS was one recombinant genome per cell and 2 pfu of HSV-1 per cell) 24 h later. Cells were collected 36 h later and centrifuged for 5 min at 2000 rpm. Media was removed and small molecular weight DNA was isolated from the pellet by Hirt extraction. Hirt extracted DNA (10 μg) was extensively digested with *Dpn*I (100 U) for 24 h. *Dpn*I does not digest newly replicated rAAV, which is not methylated after replication in eukaryotic cells. The DNA was then ethanol precipitated and analyzed on a 0.8% agarose gel for 12 h at 25V. DNA was transferred to a nylon membrane by Southern blotting. The membrane was hybridized with an [α-^{32}P] dATP-labeled *lacZ* DNA probe and exposed to film for 24 h.

The RF_m and RF_d were readily observed the positive control for rescue and replication of rAAV genomes. Rescue and replication of *Dpn*I resistant rAAV genomes from transfected plasmids was also observed where pAAVlacZ transfection was followed by HSV-RC/KOS superinfection. Replicative forms of rAAV were not observed in any of the other samples.

HSV-RC/KOS was also proven to rescue and amplify proviral rAAV genomes that were chromosomally integrated in the cell line UF2-293. Plates (10 cm) were seeded with 1.5×10^6 UF2-293 cells. The cells were mock infected, infected with HSV-1 (MOI of 2) or infected with HSV-RC/KOS (MOI of the HSV-RC/KOS was one recombinant genome per cell and 2 pfu of HSV-1 per cell) 24 h later. Plates were scraped 36 h post infection. Cells were centrifuged (5 min, 2000 rpm) and the media was discarded. Small molecular weight DNA was isolated from the pellet by Hirt extraction. Hirt extracted DNA (10 μg) was analyzed per well on a 0.8% agarose gel for 12 h at 25V. DNA was transferred to a nylon membrane by Southern blotting. The membrane was hybridized with an [α-^{32}P] dATP-labeled *hgfp* DNA probe, and exposed to film for 24 hours.

The replicating monomers and dimers indicative of rAAV rescue and replication were only seen in the sample containing Hirt extracted DNA from the UF2-293 cells infected with HSV-RC/KOS. Rescue of rAAV genomes from the UF2-293 cells was not due to latent wt AAV infection of the cells, which could supply Rep in *trans*. Replicative forms of rAAV were not observed in the sample in

which Hirt extracted DNA was analyzed from HSV-1 infected UF2-293 cells. If the UF2-293 cells were latently infected with wt AAV, rescue and replication of rAAV genomes would be observed in this sample. In addition, stripping of the membrane and reprobing for wt AAV replicative forms with an [α-^{32}P] dATP-labeled *cap* probe did not reveal any wt AAV replicative forms after exposure of the Southern blot for 7 days. HSV-RC/KOS was also able to rescue and replicate rAAV proviral genomes from GFP-92 cells in a similar assay with similar controls for detecting the presence of wt AAV replication.

5.4 EXAMPLE 4 - HSV-RC/KOS SUCCESSFULLY REPLICATES AND PACKAGES RAAV AT LOW EFFICIENCY

To determine if HSV-RC/KOS could replicate and package rAAV particles, and measure the efficiency of the process, the particle titers of rAAVUF2 were determined by QC-PCR™ of the rAAVUF2 prepared from UF2-293 cells using HSV-RC/KOS. UF2-293 cells (1×10^8) were infected with HSV-RC/KOS. After full CPE occurred, the cell pellet was harvested, then frozen and thawed three times. The cell lysate was then clarified and an aliquot (1/100th of the volume of the cell lysate) was treated with DNAseI and proteinase K, phenol and chloroform extracted and precipitated in ethanol. Aliquots (1 µl) of the reconstituted DNA pellet (1/20th of the volume) were then analyzed by QC-PCR™.

For the controls, either no DNA template, 100 pg p43-hgfp, 1 µl of rAAVUF2 DNA, or 50 pg of pCI-hgfpd was added to the reaction mixture. For the QC-PCR™ reactions 1µl of viral template and various amounts of internal control DNA template (pCI-hgfpd) were added to each PCR™ reaction. The amount of internal control template was 5pg, 1pg, 500fg, 100fg, or 20 fg. A 1-kb marker was run on the gel as a molecular weight standard.

The number of particles produced per cell was 2.3 +/- 0.3. The number of rAAVUF2 particles produced per cell was 100 fold lower than the number of particles usually produced per cell by transfection methods employing adenovirus superinfection.

5.5 EXAMPLE 5 – HSV-1 AMPLICON EXPRESSING REP AND CAP FROM THE P5 AND P19 PROMOTERS AND MADE WITH D27-1 HELPER VIRUS (HSV-RC/D27) SUPPORTS RESCUE AND REPLICATION OF RAAV GENOMES

The efficient replication of rAAV genomes in a lytic cycle by HSV-RC/KOS is clearly shown, as described above. Packaging of rAAV genomes by HSV-RC/KOS is extremely inefficient, however. The initial choice of wt HSV-1 as helper virus to generate HSV-RC/KOS was made because it can supply the necessary functions (early gene expression) required for wt AAV production. Unfortunately, HSV-1 induces CPE in infected cells much more rapidly than a similar infection with Ad. The rapid time course of host cell death probably limits the amount of rAAV that can be produced from each cell. Full CPE of host cells was consistently observed within 36 to 48 h after infection with HSV-1 compared to 72 to 96 h after adenoviral infection at the same MOIs. The rapidity of CPE after HSV-1 infection is due, in part, to the toxicity of the HSV-1 immediate early gene products, which are expressed within two h after infection and quickly alter the host cell's macromolecular synthesis machinery (Johnson *et al.*, 1992a; Johnson *et al.*, 1994). Host cell transcription, RNA splicing and protein synthesis are all perturbed by immediate early gene products of HSV-1 and contribute to the rapid CPE (Johnson *et al.*, 1992a; Johnson *et al.*, 1994).

An additional possible reason for the inefficiency of rAAV particle production by HSV-RC/KOS is the inhibition of host cell mRNA splicing by ICP27 (Sandri-Goldin and Mendoza, 1992). ICP27 expression would also interfere with the appropriate splicing of the AAV late p40 transcripts, which encode Cap. Decreased synthesis of Cap message in turn would limit the production of rAAV.

In order to increase the yield of rAAV produced per cell, a Rep and Cap expressing amplicon was made using the defective HSV-1 virus, d27-1. The virus d27-1 has a deletion in ICP27. Although the other immediate early proteins are expressed in d27-1 and the vector induces CPE, ICP27 itself is toxic to cells and therefore elimination of ICP27 was expected to reduce toxicity of the defective vector compared to HSV-1 (Johnson *et al.*, 1994). The ICP27 protein is also implicated in

the inhibition of mRNA splicing, and the d27-1 strain should permit more efficient and accurate splicing of the late p40 transcripts encoding Cap and increase rAAV particle yield per cell. In addition, ICP 27 is involved in the down regulation of HSV-1 early gene expression. ICP27 mutants overexpress the early gene products of HSV-1, such as ICP8, and it is these early gene products that are essential for wt AAV productive infection (McCarthy *et al.*, 1989; Rice and Knipe, 1990; Weindler and Heilbronn, 1991). Overexpression of early gene products may result in an increase in the yield of rAAV particles produced.

To determine if an HSV-1 amplicon expressing Rep and Cap and made with d27-1 helper virus could support replication and packaging of rAAV particles, HSV-RC/d27 was produced and tested in a replication assay. Dishes were seeded with 2×10^5 GFP-92 cells per well. After 24 h the cells were mock infected, infected with wt HSV-1 (MOI of 1), infected with d27-1 (MOI of 1), infected with HSV-RC/d27 (MOI of the HSV-RC/d27 was 1 recombinant genome per cell and 1 pfu of d27-1 per cell), or infected with HSV-RC/d27 (MOI of the HSV-RC/d27 was one recombinant genome per cell and one pfu of d27-1 per cell) and 12 h later superinfected with HSV-1 (MOI of 1). Plates were scraped 36 h post infection. Cells were centrifuged (5 min, 2000 rpm) and the media was discarded. Small molecular weight DNA was isolated from the pellet by Hirt extraction. Hirt extracted DNA (10 μg) was analyzed per well on a 0.8% agarose gel for 12 h at 25V. DNA was transferred to a nylon membrane by Southern blotting. The membrane was hybridized with an [α-^{32}P] dATP-labeled *hgfp* DNA probe, and exposed to film for 24 hours.

The capability of HSV-RC/d27, alone, to rescue and replicate chromosomally integrated rAAV provirus from the cell line GFP-92 was demonstrated. Coordinated expression of Rep from the amplicon and early genes from d27-1 allows replication of rAAV. Wild type levels of HSV-1 DNA synthesis and HSV-1 late gene expression are clearly not required for rAAV replication, in agreement with previous reports (Weindler and Heilbronn, 1991). Addition of HSV-1, which would provide ICP27 and allow HSV-1 DNA replication and expression of late genes to occur, does increases the amount of rAAV DNA replication.

To analyze if HSV-RC/d27 was sufficient not only to replicate but also to package rAAV in the absence of wt levels of HSV-1 DNA synthesis and late gene expression, the ability of the HSV-RC/d27 amplicon to generate rAAVUF2 DNAseI resistant particles from the cell line GFP-92 was studied. GFP-92 cells (2×10^5) were plated onto 6 well dishes. After 24 h, the cells were either not infected nor transfected, infected with Ad5 (MOI of 2), HSV-1, (MOI of 1), d27-1 (MOI of 1), HSV-RC/d27 (MOI of the HSV-RC/d27 was one recombinant genome per cell and one pfu of d27-1 per cell), or transfected with pRS5 DNA (which supplies Rep and Cap; 2μg) and superinfected with Ad5 eight h later (MOI of 2). The cells were scraped and pelleted after full CPE was observed. The cell pellet was then frozen and thawed three times in 100 μl DMEM and clarified. An aliquot of the clarified lysate (10 μl) was then DNAseI and proteinase K treated, phenol and chloroform extracted and ethanol precipitated. The DNA was pelleted and reconstituted in 20 μl dH_2O. An aliquot (2 μl) was then added to 50 μl PCR™ reactions. Aliquots of the PCR™ products (15 μl) were analyzed on a 2% agarose gel at 100V for 30 min. For the controls, either no DNA template or 200 pg p43-hgfp was added to the PCR™ reaction. A 1-kb marker was run on the gel as a molecular weight standard.

HSV-RC/d27, alone, was sufficient to produce DNAseI resistant, PCR™ detectable rAAV genomes from rAAVUF2 particles. These data support the report that neither HSV-1 DNA synthesis, nor late gene expression, is necessary for efficient AAV-2 particle production (Weindler and Heilbronn, 1991).

The CMV92gfp cell line was not latently infected with wt AAV as demonstrated by the absence of RF_m and RF_d in the study described above. If GFP-92 cells were latently infected with wt AAV, replication of rAAV genomes would have occurred when the cells were infected with HSV-1 or d27-1 alone. In addition, replicative forms of wt AAV were not detected when the membrane was stripped and probed for wt AAV sequences with an [α-^{32}P] dATP-labeled *cap* DNA probe after a 7 day exposure. In addition, no PCR™ detectable rAAV genomes were present after the cells were infected with any of the control viruses (Ad5, HSV-1 or d27-1).

5.6 EXAMPLE 6 – HSV-RC/D27 REPLICATES AND PACKAGES rAAV AS EFFICIENTLY AS STANDARD METHODS

To determine if HSV-RC/d27 could package rAAV as efficiently as transfection methods, larger scale production of rAAVUF2 was attempted. GFP-92 cells (at 60% confluency) were either transfected with pRS5 (and then superinfected with Ad5), or infected with HSV-RC/d27 (with and without superinfection with HSV-1). 6×10^7 GFP-92 cells were in each preparation. After full CPE occurred, the cell pellet was harvested, frozen, and thawed three times. The cell lysate was then clarified and an aliquot (1/1500th of the volume of the cell lysate) was treated with DNAseI and proteinase K, phenol and chloroform extracted and precipitated in ethanol.

Aliquots of the reconstituted DNA pellet (1 µl, 1/20th of the total volume) were then analyzed by QC-PCR™ to determine the number of particles produced per cell by each of the methods. For the controls, either no DNA template, 100 pg p43-hgfp, 1 µl of rAAVUF2 DNA, or 50 pg of pCI-hgfpd was added to the reaction mixture. For the QC-PCR™ reactions 1µl of viral template and various amounts of internal control DNA template (pCI-hgfpd) were added to each PCR™ reaction. The amount of internal control template was 100 pg, 25 pg, 5 pg, 1 pg, or 200 fg. A 1 kb marker was run on the gel as a molecular weight standard.

The particle production for the various methods from two independent preparations of amplicons is listed in Table 2. The data indicate that HSV-RC/d27 is almost as effective as transfection methods at producing rAAV. The yield of rAAV can be further increased by the addition of HSV-1 to the amplicon HSV-RC/d27 for the final 24 h of cell growth. The studies were done at 60% cellular confluence 24 h after seeding to maximize transfection efficiency. Cell confluency can likely be increased to 90%, as would be done during rAAV production with these amplicons, without affecting the yield per cell, thereby improving overall yield and reducing cost.

TABLE 2

EFFICIENCY OF RAAV PRODUCTION

Method	Total Cells	Preparation 1		Preparation 2	
		Total Particles	Particles/ Cell	Total Particles	Particles/ Cell
Transfection	6.5×10^7	2.4×10^{10}	400	9.0×10^9	150
HSV-RC/d27	6.5×10^7	9.0×10^9	150	1.2×10^{10}	200
HSV-RC/d27+HSV-1	6.5×10^7	1.2×10^{10}	200	3.0×10^{10}	500

5.7 EXAMPLE 7 -- RAAVUF2 GENERATED BY A REP-AND CAP-EXPRESSING AMPLICON IS INFECTIOUS

The rAAVUF2 virus prepared from the amplicon system was heat inactivated and purified on an isopycnic CsCl gradient and analyzed for its ability to transduce cells as measured by replication competence following transduction of HeLa cells.

rAAVUF2 was prepared from 6 confluent T175 flasks of UF2-293 cells (10^8 cells). Flasks were infected with HSV-RC/KOS (MOI of the HSV-RC/KOS was 2 recombinant genomes per cell and 2.5 pfu of wt HSV-1 per cell). After 48 h, rAAVUF2 was collected, heat inactivated for 1 h at 55°C and CsCl gradient purified as described. The purified rAAVUF2 (5×10^5 particles) were added to 2×10^5 HeLa cells seeded into 6 well plates 24 h earlier or the cells were mock infected. The cells were then either mock infected, infected with HSV-1 (MOI of 2.5), or infected with HSV-RC/KOS (MOI of the HSV-RC/KOS was 2 recombinant genomes per cell and 2.5 pfu of HSV-1 per cell) 24 h later. Cells were scraped 36 h later and pelleted by centrifugation (2000 rpm, 5 min). Small molecular weight DNA was isolated by Hirt extraction. Hirt extracted DNA (10 μg) was analyzed per on a 0.8% agarose gel for 12 h at 25V. DNA was transferred to a nylon membrane by Southern blotting. The membrane was probed with an [α-^{32}P] dATP-labeled *hgfp* DNA probe, and exposed to film for 24 hours.

The replicative forms indicative of infectious rAAV were produced after the cells transduced with rAAVUF2 were superinfected with HSV-RC/KOS. The RF_m

and RF_d were probably not due to transduction of the cells with a recombinant HSV vector that was generated through a recombination event of the amplicon or HSV-1 helper virus with the proviral rAAVUF2. A recombinant HSV-1 vector would not be infectious after prolonged heat inactivation and purification on a CsCl gradient.

5.8 EXAMPLE 8 - HSV-RC/D27 DOES NOT GENERATE WILD-TYPE AAV DURING THE PRODUCTION OF RAAV

A PCR™ assay was used to detect the generation of wt AAV during production of rAAV using the HSV-1 amplicons. Primers that anneal to the *D* sequence and *cap* sequence of AAV-2 only produce a product after PCR™ amplification if wt AAV is present. An aliquot of the clarified cell lysate from GFP-92 cells infected with HSV-RC/d27 or HSV-RC/d27+wt HSV-1 (1/30th of the volume of the cell lysate, preparations one and two) was treated with DNAseI and proteinase K, phenol and chloroform extracted and precipitated in ethanol. Aliquots of the reconstituted DNA pellet (9 µl, 90% of the total volume) were then analyzed for the presence of wt AAV.

As a control, DNA template was not added to one of the PCR™ reactions. A standard curve of 1 pg, 100 fg and 10 fg of pAAV2 DNA was added to three of the PCR™ reactions. Aliquots from the PCR™ reaction using DNA from preparation (prep) 1, HSV-RC/d27; prep 1, HSV-RC/d27 + HSV-1; prep 2, HSV-RC/d27 and prep 2, HSV-RC/d27 + HSV-1 were analyzed. A 123 bp DNA ladder was run on the gel as a molecular weight standard. The other 1µl from the DNA samples was analyzed for the presence of rAAVUF2 DNA using the *hgfp* primers to assure that DNA was present in the samples.

No product was detected in any of the preparations except the positive pAAV2 controls. A sensitivity of detection of 10 fg of pAAV2 in the PCR™ assay indicates that there is less that 1 wt AAV particle per 2×10^6 rAAV particles. In addition, the Southern blots described above were stripped and reprobed for the replicating forms of wt AAV using an [α-^{32}P] dATP labeled *cap* DNA probe. After exposure for 7 days, no replicative intermediates of wt AAV were observed on any of the blots.

5.9 EXAMPLE 9 – PRODUCTION OF RAAV USING A RECOMBINANT HERPES SIMPLEX VIRUS TYPE I VECTOR

The vector d27.1-rc can efficiently produce rAAV from transfected 293 cells. 293 cells were transfected with AAV-GFP proviral plasmid. Approximately 3×10^7 cells were present in each experimental group. 24 h after transfection the cells were superinfected with different MOIs of d27.1-rc. 36 h post infection, a cell lysate was Recombinant adeno-associated virus type 2 vectors (rAAV) have been extremely successful vectors for *in vivo* gene transfer. These vectors have produced long term, high-level gene expression of therapeutic proteins in immunocompetent animal models. For example, sustained production of erythropoietin from skeletal muscle after rAAV transduction has been achieved in mice (Kessler *et al.*, 1996). Therapeutic levels of Factor IX have been produced after rAAV gene transfer to the liver and skeletal muscle (Herzog *et al.*, 1997; Koeberl *et al.*, 1997; Nakai *et al.*, 1998; Monahan *et al.*, 1998). Levels of therapeutic protein production have reached up to 800 μg/ml in mice treated intramuscularly with AAV vectors expressing alpha-1 antitrypsin (Song *et al.*, 1998). Recombinant AAV vectors have been used effectively in the central nervous system (Kaplitt *et al.*, 1994; Peel *et al.*, 1997; Xiao *et al.*, 1997). In addition, rAAV has been used in human clinical trials to transfer the CFTR gene (Flotte and Carter, 1998).

Production of sufficient quantities of high-titer rAAV needed for effectiveness *in vivo* has been difficult to achieve, however. The process requires the efficient cellular delivery of the proviral construct to be packaged as rAAV, the AAV-2 *rep* and *cap* genes, as well as specific helper virus functions (Muzyczka, 1992). The proviral construct to be packaged contains the cDNA expression cassette flanked by AAV-2 inverted terminal repeats (ITRs). The ITRs are the cis acting viral DNA sequences required to direct replication and packaging of the rAAV vector (Samulski *et al.*, 1983; Hermonat and Muzyczka, 1984). AAV-2 *rep* and *cap* genes encode the four Rep proteins (Rep 78, 68, 52 and 40) involved in viral DNA replication, resolution of replicative intermediates and generation of single-strand genomes and

the three structural genes (VP1, VP2 and VP3) that make up the viral capsid (Berns, 1984; Chejanovsky and Carter, 1989; Samulski *et al.*, 1987). Usually, the proviral rAAV and the *rep* and *cap* genes are introduced into cells by plasmid transfection. Replication and packaging of rAAV then occurs after expression of specific genes from a helper virus such as adenovirus (Ad) (Berns, 1984; Carter, 1990; Huang and Hearing, 1989; Samulski and Shenk, 1988; Xiao *et al.*, 1998). Traditionally, Ad infection is used to provide helper virus functions (Muzyczka, 1992). In the case of Ad, the specific helper functions have been identified as the E1a, E1b, E2a, E4orf6 and Va RNA genes. These Ad genes encode proteins or RNA transcripts which are transcriptional regulators, and are involved in DNA replication or modify the cellular environment in order to permit efficient viral production (Berns, 1984; Carter, 1990; Huang and Hearing, 1989; Samulski and Shenk, 1988; Xiao *et al.*, 1998).

Recent improvements in rAAV packaging technology have made production of high-titer rAAV more feasible. One significant advancement has been the development of an Ad free method for rAAV production (Xiao *et al.*, 1998; Matsushita *et al.*, 1998). This method is based on transfection of a plasmid encoding the Ad helper functions required for the production of rAAV. Other improvements have included the generation of *rep* inducible cell lines, translational control of Rep production and increasing Cap expression by driving *cap* transcription with a strong heterologous promoter (Clark *et al.*, 1995; Vincent *et al.*, 1997b; Li *et al.* 1997). These improved methods still possess limitations, however. The *rep* inducible cell lines do not produce rAAV more efficiently than traditional methods. Translational and transcriptional control of Rep and Cap production do not increase the efficiency of rAAV production more than ten fold (Vincent *et al.*, 1997b; Li *et al.* 1997). The Ad free method requires successful transfection on a large scale that is not easily achieved.

While Ad is an efficient helper virus for rAAV production, little consideration has been given to other helper viruses for AAV-2 replication and packaging. Herpes simplex virus type 1 (HSV-1) is also a fully competent helper virus of AAV-2 (Rose and Koczot, 1972; Buller, 1981; Mishra and Rose, 1990; Weindler and Heilbronn,

1991). The minimal set of HSV-1 genes required for AAV-2 replication and packaging has been identified as the early genes UL5, UL8, UL52 and UL29 (Weindler and Heilbronn, 1991). These genes encode components of the HSV-1 core replication machinery- the helicase, primase and primase accessory proteins and the single-stranded-DNA binding protein (reviewed in (Knipe, 1989; Weller, 1991).

Recombinant adeno-associated virus type 2 (rAAV) vectors have recently been used to achieve long-term, high level transduction *in vivo*. Further development of rAAV vectors for clinical use requires significant technological improvements in large-scale vector production. In order to facilitate the production of rAAV vectors, a recombinant herpes simplex virus type I vector (rHSV-1) which does not produce ICP27, has been engineered to express the AAV-2 *rep* and *cap* genes. ICP27 is required for HSV-1 replication. Although *d27.1-rc* is replication defective, it does express the HSV-1 early genes required for rAAV replication and packaging (Weindler and Heilbronn, 1991; Rice and Knipe, 1990).

The vector *d27.1-rc* has been found to be as efficient at producing rAAV as Ad free methods and obviates the need for large-scale transfection protocols. In addition, the rHSV-1 vector is 100 times more efficient at producing rAAV than the amplicon system based on the HSV-1 helper functions described above. The optimal dose of this vector, *d27.1-rc*, for AAV production has been determined and results in a yield of 380 expression units (eu) of AAV-GFP produced from 293 cells following transfection with AAV-GFP plasmid DNA. In addition, *d27.1-rc* was also efficient at producing rAAV from cell lines that have an integrated AAV-GFP provirus. Up to 480 eu/cell of AAV-GFP could be produced from the cell line GFP-92, a proviral, 293 derived cell line. Effective amplification of rAAV vectors introduced into 293 cells by infection was also demonstrated. Passage of rAAV with *d27.1-rc* results in up to 200-fold amplification of AAV-GFP with each passage after coinfection of the vectors. Efficient, large-scale production ($>10^9$ cells) of AAV-GFP from a proviral cell line was also achieved and these stocks were free of replication competent AAV. The described rHSV-1 vector provides a novel, simple and flexible way to introduce the AAV-2 *rep* and *cap* genes and helper virus functions required to produce high-titer

rAAV preparations from any rAAV proviral construct. The efficiency and potential for scalable delivery of *d27.1-rc* to producer cell cultures should facilitate the production of sufficient quantities of rAAV vectors for clinical application.

9.1 METHODS

9.1.1 PLASMIDS

The plasmid pTR-UF5 is an AAV-GFP proviral construct with AAV-2 ITRs flanking both an eGFP and a neomycin resistance gene (*neo*) expression cassette. Expression of GFP is driven by the human CMV promoter. The *neo* gene is expressed from the HSV-1 *tk* promoter. The plasmid pSub201 contains the AAV-2 *rep* and *cap* genes (Samulski *et al.*, 1987). The plasmid pHSV-106 is a pBR derived plasmid into which the *Bam*HI fragment of HSV-1 (17+ stain) containing the *thymidine kinase* (*tk*) gene was cloned. The plasmid pHSV-106-*lacZ* was constructed by cloning a *lacZ* expression cassette into the *Kpn*I restriction site of pHSV-106 interrupting the *tk* gene. The plasmid pHSV-106-rc has the AAV-2 *rep* and *cap* genes from pSub201 cloned into the *Kpn*I site of pHSV-106.

9.1.2 CELL LINES

The 293 and Vero cell lines were obtained from American Type Culture Collection. The V27 cell line is a Vero derived cell line that expresses the HSV-1 ICP27 protein (Rice and Knipe, 1990). The C12 cell line is a HeLa derived cell line with inducible AAV-2 *rep* gene expression (Clark *et al.*, 1995). The GFP-92 cell line was created by infecting 293 cells with AAV-GFP, as described herein. In AAV-GFP, expression of GFP is driven by the human CMV promoter and the *neo* gene is expressed from the HSV-1 *tk* promoter. All cell lines were maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum (FBS).

9.1.3 HSV-1 VIRUSES

The virus *d27.1* is an ICP27 deletion mutant (Kos strain), which is propagated on the complementing cell line, V27 (Rice and Knipe 1990). The virus *d27.1-rc* was

constructed by first creating the *lacZ* expressing virus *d27.1-lacZ*. This β-galactosidase expressing vector was created by traditional techniques involving cotransfection of *d27.1* infected cell DNA and the integrating plasmid, pHSV-106-*lacZ* (linearized by *Bam*HI restriction digest) into V27 cells. Recombinant viruses were isolated by screening for blue plaques after agar overlay containing 400 μg/ml halogenated indolyl-β-D-galactoside (Bluogal, Gibco-BRL). Recombinant viruses were purified by three rounds of limiting dilution. Integration was confirmed by Southern analysis of restriction enzyme digested *d27.1-lacZ* infected cell DNA. The virus *d27.1-rc* was created by cotransfection of *d27.1-lacZ* infected cell DNA and the *Sph*I linearized integration plasmid pHSV-106-rc into V27 cells. Recombinant viruses were isolated by screening for white plaques after agar overlay containing 400 μg/ml Bluo-gal. Recombinant viruses were purified by three rounds of limiting dilution. Integration was confirmed by Southern analysis of restriction enzyme digested *d27.1-rc* infected cell DNA. The stability of integration with passage was assessed by isolating 10 clones of *d27.1-rc* after ten serial passages of *d27.1-rc* at a MOI of 0.1. All clones were able to rescue rAAV. Wild type HSV-1 virus capable of replicating on Vero cells was not detected in any preparation (limit of detection is < 20 plaque forming units (PFU)/ml).

9.1.4 Recombinant AAV production methods

Production of AAV-GFP from pTR-UF5 transfected 293 cells. Tissue culture dishes (10 cm) plated with 2×10^6 293 cells were transfected with 5 μg pTR-UF5 and 25 μl Lipofectamine (Gibco-BRL) as per manufacturer's instruction. Four hours post-transfection, the cells were washed and DMEM (10% FBS) was added. Twenty hours later, the cells were superinfected with *d27.1-rc* at different MOIs or *d27.1-lacZ* at a MOI of 10. (The cells on an extra transfected dish were trypsinized, resuspended and counted using a haemocytometer.) Approximately 3.5×10^7 cells were infected per MOI. Forty-eight hours later, the cells were harvested and pelleted by centrifugation (1500 rpm, 5 minutes). The cells were then resuspended in 10 ml of DMEM and cell associated rAAV was released by three rounds of freezing and thawing. Cell debris

was pelleted by centrifugation (1000 rpm, 5 minutes). The cell lysates were then titered for expression units of AAV-GFP as described below and purified by CsCl gradient (Kessler *et al.*, 1996). This experiment was repeated in triplicate.

9.1.5 PRODUCTION OF AAV-GFP FROM THE CELL LINE GFP-92

The GFP-92 cells were plated in 75 cm^2 tissue culture flasks. Twelve hours later, the cells were infected with *d27.1-rc* at different MOIs or *d27.1-lacZ* at a MOI of 10. The number of cells in one extra flask was determined as described above. Approximately 1.5×10^7 GFP-92 cells were infected per MOI. Cells were harvested 48h post-infection and cell associated AAV-GFP was processed and titered as described above. This experiment was repeated in triplicate.

9.1.6 PRODUCTION OF AAV-GFP BY AMPLIFYING AAV-GFP VIA INFECTION

293 cells (1.5×10^6 cells) were plated in six well tissue culture dishes. Twelve hours later, the cells were infected with AAV-GFP at different MOIs. Twelve hours later, the cells were infected with *d27.1-rc* at a MOI of 10. Cells were harvested 48 h post-infection and cell associated AAV-GFP was processed as described above. This experiment was repeated in triplicate. The amount of output rAAV was determined using the fluorescent cell assay described below.

9.1.7 LARGE-SCALE AAV-GFP PRODUCTION

GFP-92 cells were plated on 175 cm^2 tissue culture flasks 12 h prior to infection. 1×10^9 GFP-92 cells were infected 12 h later with *d27.1-rc* at a MOI of 10. Cells were harvested 48 h post-infection and cell associated AAV-GFP was processed as described above. This experiment was repeated in duplicate. Stocks were analyzed for replication competent AAV (rcAAV) (Koeberl *et al.*, 1997). Replication competent AAV was not detected (limit of detection was one replication unit per 10^7 gfp expression units).

9.1.8 TITERING OF AAV-GFP IN THE VIRAL LYSATES BY THE FLUORESCENT CELL ASSAY

Viral lysates were heat inactivated (55°C, one h). Serial dilutions of AAV-GFP were then titered on C12 cells with Ad coinfection (MOI of 20) (Clark *et al.*, 1996). The cells were then analyzed for GFP expression using fluorescence microscopy at 48h post-infection.

9.1.9 WESTERN ANALYSIS OF AAV-2 REP PROTEINS

The indicated cells (approximately 4×10^6 cells) were plated onto 6 cm tissue culture plates 12 h before infection with *d27.1-rc* (MOI as indicated). Control samples not infected. Cells were harvested 48 h post-infection and cell lysates were made and loaded on a 10% sodium dodecyl sulfate (SDS)-polyacrylamide gel followed by immunoblotting using a monoclonal antibody (clone 1F11.8, 1:5000 dilution) that recognizes all four AAV-2 Rep proteins. The antibody was detected by chemiluminescence (Amersham).

9.1.10 IMMUNOFLUORESCENCE ASSAY

Cells (293, Vero or V27 cells) were plated onto a two-well tissue culture slides at a density of 1.5×10^5 cells per well. For the anti-AAV Rep immunofluorescence assay, 293 cells were infected 12h later with *d27.1-rc* at a MOI of 10. Cells were washed with DMEM after a 45 minute adsorption period and DMEM with 10% FBS was then added. After 10 h, cells were washed twice with PBS and fixed for 10 minutes in 4% paraformaldehyde in PBS. Cells were washed twice with PBS and permeabilized with 0.2% Triton X-100 in PBS for two minutes. Cells were then washed twice with PBS and incubated for one hour at 37°C in a humidified chamber with monoclonal anti-Rep antibody (American Research Products, clone 226.7, 1:1 dilution). This antibody recognizes all four Rep proteins. The cells were then washed three times with PBS and incubated for 30 minutes at 37°C with FITC conjugated, donkey-anti-mouse secondary antibody (diluted 1:100 in 2% goat serum, 2% donkey serum in PBS). The slides were then washed three times, covered with a 4',6-

diamidino-2-phenylindole (DAPI) containing mounting solution (Vector Laboratories), sealed and analyzed for immunofluorescence. Microscopy was performed on a Leitz microscope with Image Pro acquisition equipment and image analysis software.

To analyze the maturation of HSV-1 viral replication centers and Rep expression in V27 cells after *d27.1-rc* infection, a rabbit polyclonal anti-ICP8 (the HSV-1 single-stranded-DNA binding protein) antibody (PAb 3-83) and the monoclonal anti-Rep antibody (American Research Products, clone 226.7, 1:1 dilution) were utilized in a double label experiment. All procedures were as previously described except that V27 cells were infected at a MOI of one. After fixing and permeablization, V27 cells were incubated as above with the anti-Rep monoclonal antibody. The cells were then washed twice with PBS and incubated with the anti-ICP8 antibody (diluted 1:50 in 2% goat serum, 2% donkey serum in PBS) for one hour in a humidified chamber at 37°C. The cells were then washed three times with PBS and then incubated with a rhodamine conjugated, donkey-anti-rabbit secondary antibody and FITC conjugated, donkey-anti-mouse secondary antibody (both diluted 1:100 in 2% goat serum, 2% donkey serum in PBS) for 30 minutes at 37°C. The slides were then washed three times, covered with DAPI containing mounting solution, sealed and analyzed for immunofluorescence. Vero cells were infected and processed along side V27 cells to serve as positive controls for Rep staining.

9.2 RESULTS

9.2.1 CONSTRUCTION AND CHARACTERIZATION OF *D27.1-RC*

The rHSV-1, *d27.1-rc* was constructed by homologous recombination of the AAV-2 *rep* and *cap* genes into the *tk* locus of the rHSV-1 virus *d27.1* (FIG. 2). In this recombinant virus, the AAV-2 *rep* and *cap* genes are under control of their native promoters- the p5, p19 and p40 promoters. The p5, p19 and p40 promoters drive expression of the AAV-2 proteins Rep 78 and 68, Rep 52 and 40, and the capsid structural proteins VP1, VP2 and VP3, respectively (Carter *et al.*, 1983; Green and

Roeder, 1980; Laughlin *et al.*, 1979; Lusby *et al.*, 1980; Marcus *et al.*, 1981). Homologous recombination into the *tk* gene was confirmed by Southern blot analysis of restriction digests of *d27.1-rc* infected cell DNA. In addition, *d27.1-rc* plaque formation on V27 cells, a complementing cell line, was not affected by 5-bromo-deoxycytidine. This indicates that the *tk* gene, appropriately, did not produce functional thymidine kinase.

9.2.2 PRODUCTION OF AAV-2 REP BY *D27.1-RC*

In order for *d27.1-rc* to replicate rAAV, the AAV-2 Rep proteins must be efficiently expressed and localized to the nucleus of the cell after *d27.1-rc* infection. To determine the level of expression of the AAV-2 Rep proteins from *d27.1-rc*, Western analysis was utilized. The expression of the AAV-2 Rep proteins from *d27.1-rc* after infection of three different cell lines (293, Vero and V27 cells) at different multiplicities of infection (MOI; 0, 0.1, 1 and 5 infectious units/cell) was analyzed.

The vector *d27.1-rc* expressed different levels of each of the AAV-2 Rep proteins in the different cell lines. In 293 cells, high level expression of all four Rep proteins occurred after infection with *d27.1-rc*. Expression of the Rep proteins was also observed in Vero cells after *d27.1-rc* infection. In contrast, only a small amount of Rep was produced in V27 cells after *d27.1-rc* infection, especially at higher MOIs. The level of Rep expression after *d27.1-rc* infection of 293 and Vero cells was observed to be dependent on the MOI. The higher level expression of Rep in 293 cells after *d27.1-rc* infection may be due to upregulation of the p5 promoter by Ad E1a present in 293 cells. The low level of Rep expressed in V27 cells after *d27.1-rc* infection in part results from lytic replication of *d27.1-rc* after infection of this cell line.

9.2.3 THE REP PRODUCED BY *D27.1-RC* LOCALIZES TO THE NUCLEUS

The cellular distribution of the AAV-2 Rep proteins was determined in an immunofluorescence assay (IFA) which utilized a monoclonal antibody that

recognizes the four Rep proteins. The IFA was conducted 10 h after infection of 293 cells with *d27.1-rc*. The 293 cells were processed for IFA and the cells were incubated with a monoclonal antibody that detects all four Rep proteins (78, 68, 52, and 40). The cells were then incubated with a FITC conjugated, donkey-anti-mouse secondary antibody.

The Rep proteins, expressed after infection of 293 cells by *d27.1-rc*, localized to discrete nuclear punctate bodies. The distribution of Rep proteins to the nucleus of 293 cells infected with *d27.1-rc* is a prerequisite for rAAV replication.

9.2.4 REPLICATION CENTER FORMATION BY *D27.1-RC*

The observation has been made that the *rep* gene products are capable of inhibiting viral and cellular DNA replication (Khleif *et al.*, 1991; Heilbronn *et al.*, 1990; Weitzman *et al.*, 1996a). In particular, *rep* gene products have been shown to be potent inhibitors of Ad DNA replication and prevent the maturation of Ad DNA replication centers (Weitzman *et al.*, 1996b). This inhibitory effect of Rep proteins is presumably responsible for the inability to generate a recombinant Ad that expresses the AAV-2 *rep* gene. If *rep* gene products similarly inhibited HSV-1 viral DNA replication, the recombinant virus, *d27.1-rc*, would not be able to propagate. Replication of *d27.1-rc* was not affected by the presence of the *rep* gene, however. The kinetics of plaque formation on V27 cells, the complementing cell line, and the amount of virus produced per cell was identical to the parent virus, *d27.1*.

In addition, the development of HSV-1 DNA replication centers after *d27.1-rc* infection of V27 cells was not affected by the presence of the *rep* gene. HSV-1 replication centers develop in the nuclei of infected cells in a time dependent manner (Quinlan *et al.*, 1984). Viral and cellular proteins required for viral DNA replication (such as the HSV-1 core replication proteins which includes ICP8, the single-stranded-DNA binding protein) and replicating viral DNA localize to these centers (Quinlan *et al.*, 1984; Liptak *et al.*, 1996; Lukonis and Weller, 1996; Zhong and Hayward, 1997).

The immunofluorescence assay showing the development of mature HSV-1 viral DNA replication centers and minimal Rep expression in V27 cells after infection with *d27.1-rc* was conducted as follows. Twelve hours after infection (MOI of 1), V27 cells were processed for IFA and incubated with a rabbit, anti-ICP8 antibody and a monoclonal, anti-Rep antibody. The cells were then incubated with a rhodamine conjugated, donkey-anti-rabbit secondary antibody and a FITC conjugated, donkey-anti-mouse secondary antibody.

Mature HSV-1 replication centers were observed in the nuclei of V27 cells 12 h after *d27.1-rc* infection, as indicated by the distribution of ICP8. This distribution of ICP8 is characteristic of fully developed HSV-1 replication centers (Zhong and Hayward, 1997) and did not differ from replication centers formed in V27 cells by the parent virus, *d27.1*. In addition, minimal AAV-2 Rep expression was observed in V27 cells after *d27.1-rc* infection.

9.2.5 THE VECTOR *D27.1-RC* IS EFFICIENT AT PRODUCING INFECTIOUS RAAV FROM DIFFERENT RAAV PROVIRAL TEMPLATES

To determine the flexibility and efficiency of rAAV production using *d27.1-rc*, the production of rAAV from proviral plasmid transfected into cells, from a proviral cell line and by amplifying rAAV by coinfection was studied. The vector *d27.1-rc* was observed to effectively rescue rAAV from pTR-UF5 transfected 293 cells. The plasmid pTR-UF5 contains a proviral rAAV genome that encodes the green fluorescent protein (GFP) (Zolotukhin *et al.*, 1996).

The purified AAV-GFP produced by *d27.1-rc* was shown to be infectious. C12 cells were infected with the AAV-GFP (MOI of 5 eu) produced by *d27.1-rc*. The cells were then coinfected with Ad (MOI of 20). Fluorescent microscopy was used to detect GFP expression 24h after infection. Transfection of 293 cells with pTR-UF5 followed by super-infection with *d27.1-rc* resulted in rescue of infectious AAV-GFP (FIG. 3). The amount of AAV-GFP produced was a function of the MOI of *d27.1-rc*. An increase in the yield of AAV-GFP was observed up to an MOI of 10. At this MOI, the yield of AAV-GFP was 381 eu/cell. This level of production compares

favorably with recently developed rAAV production protocols based upon Ad free transfection procedures (Xiao *et al.*, 1998; Matsushita *et al.*, 1998). Infection of pTR-UF5 transfected 293 cells with a control virus, *d27.1-lacZ*, at an MOI of 10 did not produce AAV-GFP.

The vector *d27.1-rc* was also capable of efficient AAV-GFP production from the cell line GFP-92 (FIG. 4). In the cell line GFP-92, a proviral rAAV genome that encodes GFP is integrated into the chromosomal DNA. As in the transfection experiment, the amount of AAV-GFP produced was observed to be a function of the MOI of *d27.1-rc*. At the most efficient MOI for AAV-GFP replication and packaging, 480 eu/cell was produced using the vector *d27.1-rc*. Infection of this cell line with the control virus *d27.1-lacZ* at an MOI of 10 did not produce AAV-GFP.

9.2.6 AMPLIFICATION OF RAAV VIA CO-INFECTION WITH RHSV

Interestingly, *d27.1-rc* can also be used to amplify rAAV genomes introduced into cells by infection of rAAV (Table 3). 293 cells were infected with different MOIs of AAV-GFP as indicated. 12 h after infection, the cells were superinfected with *d27.1-rc* at a MOI of 10. 48 h post-infection a cell lysate was made from the infected cells by three rounds of freeze-thaw. The viral lysate was heat inactivated at 55°C for one hour and then titered in duplicate on C12 cells that were coinfected with adenovirus (MOI of 20). 48 h post-infection the C12 cells were analyzed for GFP expression using fluorescent microscopy and a titer was determined (expression units). The data represents duplicate experiments.

TABLE 3

SERIAL PASSAGE OF RAAV WITH *D27.1-RC* RESULTS IN VECTOR AMPLIFICATION

Passage Number	Input Vector	Output Vector	Fold Amplification	Total Amplification
1	5.0×10^3	1.0×10^6	200	200
2	1.0×10^4	1.75×10^6	175	3.5×10^4
3	1.75×10^4	2.97×10^7	170	5.95×10^6

When rAAV and rHSV are co-infected in 293 cells amplification of rAAV genomes is observed. Infection with *d27.1-rc* (MOI of 10) along with rAAV (MOI of 0.1) leads to a 200 fold amplification of input AAV-GFP. The total amplification of rAAV was greater than 10^6 after three cycles of passage. While not as efficient as the production of AAV-GFP from transfected plasmid or a proviral cell line, coinfection of rAAV vectors with *d27.1-rc* permits serial amplification of rAAV *via* scaleable infection.

9.2.7 THE EFFICIENCY OF RAAV PRODUCTION BY *D27.1-RC* IS MAINTAINED WHEN THE SCALE OF PRODUCTION IS INCREASED

To verify that *d27.1-rc* can be utilized to produce rAAV on a larger scale, 10^9 GFP-92 cells were infected with *d27.1-rc* (Table 4).

TABLE 4

EFFICIENT LARGE-SCALE PRODUCTION OF RAAV IS OBSERVED USING *D27.1-RC*

Study Number	Number of GFP-92 cells	Amount of virus produced in cell lysate (eu)	Expression units produced per cell
1	1.0×10^9	3.8×10^{11}	380
2	1.1×10^9	3.7×10^{11}	338

The yield of AAV-GFP, 380 eu/cell and 338 eu/cell in duplicate experiments, indicates that *d27.1-rc* is able to efficiently produce rAAV after the scale of infection is increased. Maintaining efficient rAAV production as the scale of *d27.1-rc* infection is increased is required for *d27.1-rc* to be a viable method for large-scale production of rAAV.

9.3 Recombinant HSV Vector Expressing AAV Rep and Cap Results in High-Titer rAAV Production

Recombinant adeno-associated virus mediated gene transfer has been uniquely successful in achieving long-term, high-level gene expression *in vivo*. Many potential applications for the use of rAAV in genetic disease require a substantial vector dose to achieve a therapeutic effect. One significant problem associated with rAAV vectors, has been the difficulty in generating sufficient quantities of high-titer vector required for *in vivo* applications. This difficulty has led to improvements in numerous aspects of rAAV vector development in order to increase the efficiency of rAAV production. These strategies have all involved the use of adenovirus to provide the helper functions for rAAV production, however. Few studies have explored the possibility of using other helper viruses of AAV-2 replication and packaging for large-scale production.

This Example describes the development of an alternative system for production of rAAV. This system is based upon the HSV-1 helper functions of AAV-2 replication and packaging. By generating a recombinant HSV-1 encoding the AAV-2 *rep* and *cap* genes, a single infectious helper has been created. The expression of Rep from this vector appears to be regulated and is appropriately distributed to the nucleus. The rHSV-1, *d27.1-rc*, propagates readily and its replication is not affected by the presence of *rep*.

Development of mature HSV-1 replication centers in the presence of *rep* appears to be unique to this vector. One possible explanation why the presence of the *rep* gene did not affect the kinetics of *d27.1-rc* replication or the formation of mature viral replication centers is that Rep proteins are not efficiently expressed in the V27 cells after *d27.1-rc* infection. Both Western analysis and an IFA were used to analyze Rep expression in 293, Vero and V27 cells after *d27.1-rc* infection. By Western analysis, high level Rep expression was observed in 293 cells and Vero cells but not in V27 cells after infection with *d27.1-rc*. By IFA, Rep expression was observed in the nucleus of infected 293 cells and Vero cells after infection with *d27.1-rc*, but not in V27 cells. The minimal Rep expression after *d27.1-rc* infection of V27 cells may

explain how generation of *d27.1-rc* was feasible and why similar efforts to construct recombinant Ad vectors with the *rep* gene have failed.

The *d27.1* vector was chosen as the mutant background to provide the viral helper functions for several reasons. The vector *d27.1* has a mutation in the immediate early gene IE63 and does not produce ICP27 (Rice and Knipe, 1990). The protein ICP27 has been implicated in the inhibition of host cell mRNA splicing (Sandri-Goldin and Mendoza, 1992; McLauchlan *et al.*, 1992). The use of *d27.1* minimizes inhibition of splicing of the *rep* and *cap* messages compared to a vector which produces ICP27. In addition, *d27.1* overexpresses ICP8 (Rice and Knipe, 1990), one of the HSV-1 genes essential for AAV-2 replication (Weindler and Heilbronn, 1991). High level expression of ICP8, the single-stranded DNA binding protein, is beneficial for rAAV production.

The most efficient manner in which *d27.1-rc* is used for large scale rAAV production involves infection of a proviral cell line that provides the rAAV template to be packaged. In this two-part system, the proviral cell line is grown at high densities in large quantities in spinner cultures or cartridge systems. The AAV-2 *rep* and *cap* genes and the helper functions required for rAAV production are then provided by *d27.1-rc* infection. Using *d27.1-rc* to infect the proviral cells eliminates the need for transfection at any step in the production process. The choice of cell line used for this system is important, however. The results of Western analysis indicate that *d27.1-rc* efficiently expresses the AAV-2 Rep proteins only in certain cell lines.

The dose response curve for the production of AAV-GFP by *d27.1-rc* demonstrates that increasing the MOI of *d27.1-rc* augments rAAV production to a point. The vector *d27.1-rc* still expresses the immediate early genes that encode the viral proteins ICP0 and ICP4 (Rice and Knipe, 1990). Expression of these immediate early genes is detrimental to the cell and induces cell death (Johnson *et al.*, 1992b; Johnson and Curtis, 1994). At high MOIs, increased expression of these immediate early genes probably leads to rapid cell death, limiting the production of rAAV. At a MOI of 25, while there is increased expression of the AAV-2 *rep* genes and the HSV-1 helper genes necessary for rAAV production, increased cytotoxicity due to

additional gene expression from the vector also occurs. At a MOI of 10, the most effective balance exists between expression of the AAV-2 *rep* and *cap* genes and HSV-1 helper functions required for rAAV production and the cytotoxicity inherent to the vector.

Replication of HSV-1 is not required for efficient replication and packaging of AAV-2 (Weindler and Heilbronn, 1991). Cells lines such as 293 cells, which do not complement *d27.1-rc* replication, can therefore be used to produce rAAV. Using a non-complementing cell line to produce rAAV permits the production of rAAV without generating additional *d27.1-rc*. The helper virus, *d27.1-rc,* is therefore effectively eliminated from the rAAV produced.

The application of a recombinant virus to introduce the AAV-2 *rep* and *cap* and helper virus functions into cells in order to produce rAAV has certain advantages over the amplicon system described above. Unlike a recombinant HSV-1 vector, an amplicon system has a variable helper virus to amplicon virus ratio from passage to passage. This variability makes optimization of an amplicon system for rAAV production difficult since the ratio of helper virus to amplicon virus effects the amount of rAAV produced. In addition, there is no selective pressure to maintain the recombinant AAV-2 genome in the amplicon. With passage, deletion and recombination of the amplicon genome is likely to occur, resulting in decreased efficiency of rAAV production after serial passage of the amplicon. These problems are not encountered using the recombinant virus *d27.1-rc*.

Large-scale production of rAAV vectors is required for *in vivo* preclinical and clinical trials of potentially therapeutic rAAV vectors. The vector *d27.1-rc* facilitates the production of rAAV. The vector *d27.1-rc* is flexible and can be utilized to produce rAAV from transfected cells, cell lines or even infected rAAV. The rescue of rAAV from proviral cell lines at or above the efficiency of Ad free methods permits large-scale production of rAAV without requiring a transfection procedure. Combined with recently developed purification procedures (Xiao *et al.*, 1998, Grimm *et al.*, 1998, Zolotukhin *et al.*, 1999), *d27.1-rc* is an attractive way to produce the large quantity of rAAV that is needed for clinical success of rAAV based gene therapy.

6.0 REFERENCES

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All of the compositions and/or methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and/or methods, and in the steps or in the sequence of steps of the methods described herein, without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents that are both chemically and physiologically related may be substituted

for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

WHAT IS CLAIMED IS:

1. A recombinant herpes simplex virus vector comprising an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter.

2. The recombinant vector of claim 1, wherein said AAV *rep* coding sequence or said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

3. The recombinant vector of claim 2, wherein said AAV *rep* coding sequence and said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

4. The recombinant vector of claim 1, in which a non-essential HSV gene is altered.

5. The recombinant vector of claim 4, in which a non-essential HSV gene is altered to increase expression.

6. The recombinant vector of claim 5, in which said non-essential HSV gene encodes ICP8.

7. The recombinant vector of claim 4, in which a non-essential HSV gene is mutated or substantially deleted.

8. The recombinant vector of claim 7, in which a non-essential HSV gene is substantially deleted.

9. The recombinant vector of claim 8, in which said non-essential HSV gene encodes ICP27 or glycoprotein H.

10. The recombinant vector of claim 9, in which said non-essential HSV gene encodes ICP27.

11. The recombinant vector of claim 1, comprised within a recombinant herpes simplex virus.

12. A recombinant herpes simplex virus comprising an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter.

13. The recombinant virus of claim 12, wherein said AAV *rep* coding sequence or said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

14. The recombinant virus of claim 13, wherein said AAV *rep* coding sequence and said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

15. The recombinant virus of claim 12, in which a non-essential HSV gene is altered.

16. The recombinant virus of claim 15, in which a non-essential HSV gene is altered to increase expression.

17. The recombinant virus of claim 16, in which said non-essential HSV gene encodes ICP8.

18. The recombinant virus of claim 12, in which a non-essential HSV gene is mutated or substantially deleted.

19. The recombinant virus of claim 18, in which a non-essential HSV gene is substantially deleted.

20. The recombinant virus of claim 19, in which said non-essential HSV gene encodes ICP27 or glycoprotein H.

21. The recombinant virus of claim 20, in which said non-essential HSV gene encodes ICP27.

22. The recombinant virus of claim 21, wherein said recombinant virus is the *d27.1rc* virus.

23. A kit comprising, in a suitable container, a DNA segment comprising an AAV *rep* coding sequence operably linked to a promoter, an AAV *cap* coding sequence operably linked to a promoter, an HSV-1 origin of replication and an HSV-1 packaging sequence.

24. The kit of claim 23, further comprising an HSV-1 helper virus.

25. The kit of claim 24, in which a non-essential gene of said HSV-1 helper virus is altered.

26. The kit of claim 25, in which a non-essential gene of said HSV-1 helper virus is altered to increase expression.

27. The kit of claim 26, in which said non-essential gene of said HSV-1 helper virus encodes ICP8.

28. The kit of claim 25, in which a non-essential gene of said HSV-1 helper virus is mutated or substantially deleted.

29. The kit of claim 28, in which a non-essential gene of said HSV-1 helper virus is substantially deleted.

30. The kit of claim 29, in which said non-essential gene of said HSV-1 helper virus encodes ICP27 or glycoprotein H.

31. The kit of claim 30, in which said non-essential gene of said HSV-1 helper virus encodes ICP27.

32. The kit of claim 31, wherein said HSV-1 helper virus is the d27.1 HSV-1 virus.

33. A kit comprising, in a suitable container, a recombinant herpes simplex virus vector comprising an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter.

34. The kit of claim 33, wherein said recombinant herpes simplex virus vector is comprised in a recombinant herpes simplex virus.

35. The kit of claim 34, in which a non-essential gene of said recombinant herpes simplex virus is altered.

36. The kit of claim 35, in which a non-essential gene of said recombinant herpes simplex virus is altered to increase expression.

37. The kit of claim 36, in which said non-essential gene of said recombinant herpes simplex virus encodes ICP8.

38. The kit of claim 35, in which a non-essential gene of said recombinant herpes simplex virus is mutated or substantially deleted.

39. The kit of claim 38, in which a non-essential gene of said recombinant herpes simplex virus is substantially deleted.

40. The kit of claim 39, in which said non-essential gene of said recombinant herpes simplex virus encodes ICP27 or glycoprotein H.

41. The kit of claim 40, in which said non-essential gene of said recombinant herpes simplex virus encodes ICP27.

42. The kit of claim 41, wherein said recombinant herpes simplex virus is the *d27.1rc* HSV-1 virus.

43. A method for preparing a rAAV comprising:

a) providing an HSV-1 helper virus and a DNA segment comprising an AAV *rep* coding sequence operably linked to a promoter, an AAV *cap* coding sequence operably linked to a promoter, an HSV-1 origin of

replication and an HSV-1 packaging sequence to a host cell that comprises a rAAV;

b) culturing said cell under conditions effective to produce rAAV in said cell; and

c) obtaining said rAAV from said cell.

44. The method of claim 43, wherein said host cell comprises said rAAV integrated into the genome of said cell.

45. The method of claim 43, wherein said host cell is provided with said rAAV, said HSV-1 helper virus and said DNA segment simultaneously.

46. The method of claim 43, wherein said host cell is a HeLa, 293 or Vero cell.

47. The method of claim 43, wherein said rAAV comprises an AAV-2 genome.

48. The method of claim 43, wherein said rAAV comprises an AAV-1, AAV-2, AAV-3, AAV-4, AAV-5 or AAV-6 capsid.

49. The method of claim 43, wherein said rAAV comprises a therapeutic gene.

50. The method of claim 43, wherein said AAV *rep* coding sequence or said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

51. The method of claim 50, wherein said AAV *rep* coding sequence and said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

52. The method of claim 43, in which a non-essential gene of said HSV-1 helper virus is altered.

53. The method of claim 52, in which a non-essential gene of said HSV-1 helper virus is altered to increase expression.

54. The method of claim 53, in which said non-essential gene of said HSV-1 helper virus encodes ICP8.

55. The method of claim 52, in which a non-essential gene of said HSV-1 helper virus is mutated or substantially deleted.

56. The method of claim 55, in which a non-essential gene of said HSV-1 helper virus is substantially deleted.

57. The method of claim 56, in which said non-essential gene of said HSV-1 helper virus encodes ICP27 or glycoprotein H.

58. The method of claim 57, in which said non-essential gene of said HSV-1 helper virus encodes ICP27.

59. The method of claim 58, wherein said HSV-1 helper virus is the d27.1 HSV-1 virus.

60. A recombinant AAV virus produced by the method of claim 43.

61. A kit comprising, in a suitable container, a recombinant AAV virus produced by the method of claim 43.

62. A method for preparing a rAAV comprising:

a) providing a recombinant herpes simplex virus that comprises an AAV *rep* coding sequence operably linked to a promoter and an AAV *cap* coding sequence operably linked to a promoter to a host cell that comprises a rAAV;

b) culturing said cell under conditions effective to produce rAAV in said cell; and

c) obtaining said rAAV from said cell.

63. The method of claim 62, wherein said host cell comprises said rAAV integrated into the genome of said cell.

64. The method of claim 62, wherein said host cell is provided with said rAAV and said recombinant herpes simplex virus simultaneously.

65. The method of claim 62, wherein said host cell is a HeLa, 293 or Vero cell.

66. The method of claim 62, wherein said rAAV comprises an AAV-2 genome.

67. The method of claim 62, wherein said rAAV comprises an AAV-1, AAV-2, AAV-3, AAV-4, AAV-5 or AAV-6 capsid.

68. The method of claim 62, wherein said rAAV comprises a therapeutic gene.

69. The method of claim 62, wherein said AAV *rep* coding sequence or said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

70. The method of claim 69, wherein said AAV *rep* coding sequence and said AAV *cap* coding sequence is operably linked to a p5, p19 or p40 promoter.

71. The method of claim 62, in which a non-essential gene of said recombinant herpes simplex virus is altered.

72. The method of claim 71, in which a non-essential gene of said recombinant herpes simplex virus is altered to increase expression.

73. The method of claim 72, in which said non-essential gene of said recombinant herpes simplex virus encodes ICP8.

74. The method of claim 71, in which a non-essential gene of said recombinant herpes simplex virus is mutated or substantially deleted.

75. The method of claim 74, in which a non-essential gene of said recombinant herpes simplex virus is substantially deleted.

76. The method of claim 75, in which said non-essential gene of said recombinant herpes simplex virus encodes ICP27 or glycoprotein H.

77. The method of claim 76, in which said non-essential gene of said recombinant herpes simplex virus encodes ICP27.

78. The method of claim 77, wherein said recombinant herpes simplex virus is the *d27.1rc* HSV-1 virus.

79. A recombinant AAV virus produced by the method of claim 62.

5

80. A kit comprising, in a suitable container, a recombinant AAV virus produced by the method of claim 62.

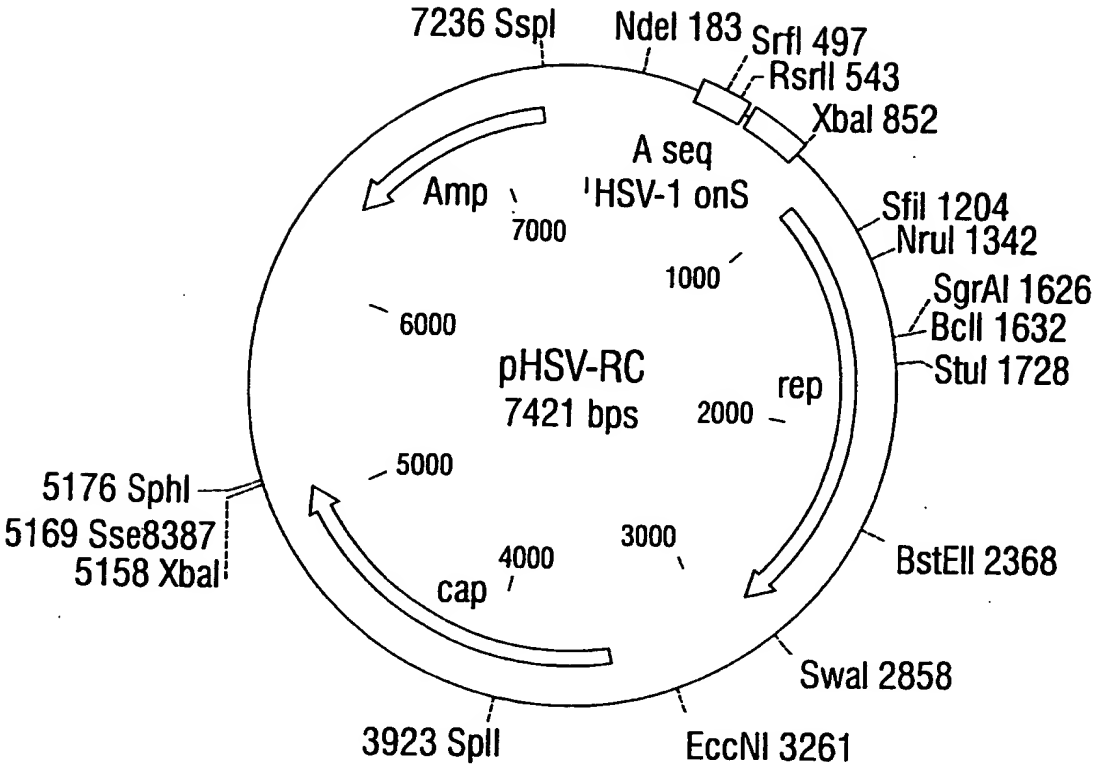
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FIG. 1

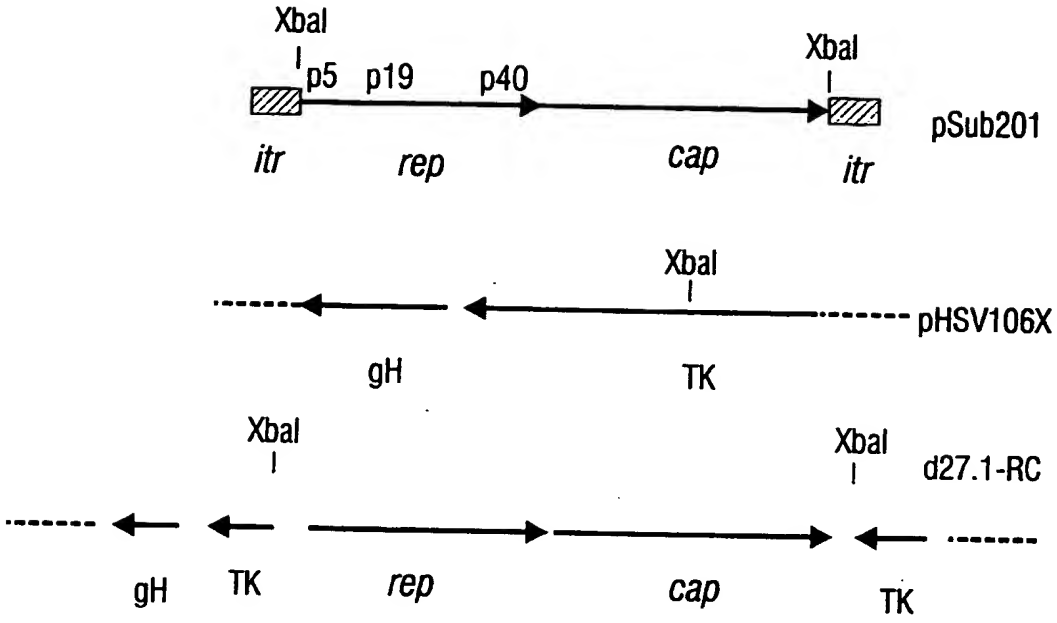
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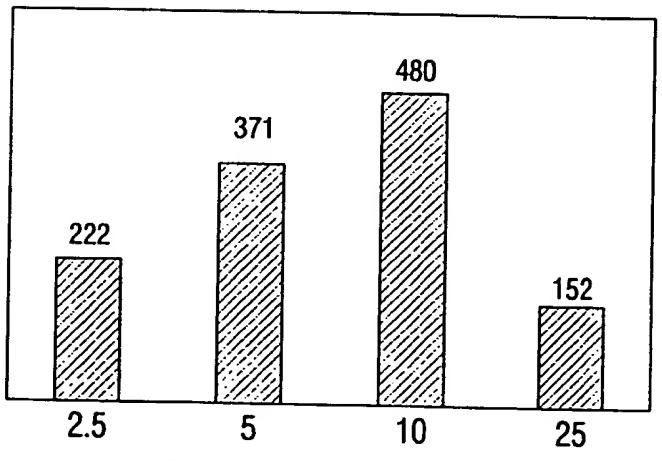
FIG. 2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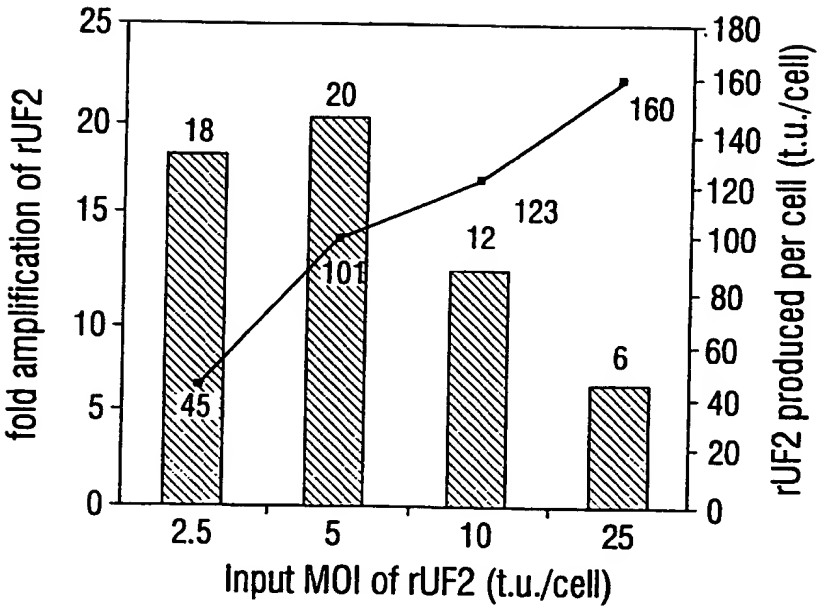
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140
120
100
80
60
40
20
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123
160
2.5
5
10
25
Input MOI of rUF2 (t.u./cell)

FIG. 4

SEQUENCE LISTING

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Muzyczka, Nicholas
Zolotukhin, Sergei

<120> METHODS FOR LARGE-SCALE PRODUCTION OF RECOMBINANT AAV VECTORS

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PCT

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Mit internationalem Recherchenbericht.

(54) Title: RECOMBINANT HERPES VIRUSES FOR PREPARING RECOMBINANT ADENO–ASSOCIATED VIRUSES

(54) Bezeichnung: REKOMBINANTE HERPESVIREN FÜR DIE ERZEUGUNG REKOMBINANTER ADENO–ASSOZIIERTER–VIREN

(57) Abstract

The invention relates to a recombinant herpes virus which contains the rep and cap genes of the adeno–associated virus, and to a method for producing high–titre, highly infectious adeno–associated virus vector preparations.

(57) Zusammenfassung

Es wird ein rekombinanter Herpesvirus beschrieben, der die rep– und cap–Gene von AAV umfaßt sowie ein Verfahren zur Herstellung von hochtitrigen, hochinfektiösen Adeno–assoziierten Virus–Vektor–Präparationen.

LEDIGLICH ZUR INFORMATION

Codes zur Identifizierung von PCT-Vertragsstaaten auf den Kopfbögen der Schriften, die internationale Anmeldungen gemäss dem PCT veröffentlichen.

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Rekombinante Herpesviren für die Erzeugung rekombinanter Adeno-assoziierter-Viren

Beschreibung

Die Erfindung betrifft einen rekombinanten Herpesvirus, ein Verfahren zur dessen Herstellung sowie ein Verfahren zur Herstellung von hochtitrigen, infektiösen Adeno-assoziierten Virus-Vektor-Präparationen.

Es sind zahlreiche genetische Erkrankungen bekannt, für die bisher keine wirksame Therapie gefunden wurde. Ein möglicher Weg zur Behandlung genetischer Erkrankungen besteht darin, ein bestimmtes Gen, welches die genetische Erkrankung korrigieren kann, in das Genom des Patienten einzubringen, so daß es in der DNA des Patienten vorliegt und sich dort replizieren kann.

Zum Einbringen des gewünschten korrigierenden Gens in die Zelle können Vektoren verwendet werden, wobei virale Vektoren auf der Basis von Adeno-assoziierten Viren (AAV) für die Gentherapie gegenüber anderen viralen Vektorsystemen eine Reihe von Vorteilen aufweisen. AAV ist ein sehr stabiles, aber apathogenes Virus. Zudem hat es einen breiten Gewebetropismus und die Fähigkeit zur effizienten chromosalen Integrationen sowohl in proliferierenden als auch in ruhenden Zellen.

Als virale Vektorsysteme werden zumeist AAV-Vektoren auf Basis des Adeno-assoziierten Virus Typ 2 (AAV-2) eingesetzt (Carter, Curr. Opinion. Biotech. 3 (1992) 533; Muzyczka, Curr. Top. Microbiol. Imm. 158 (1992) 97). Bei AAV-2 handelt es sich um ein weit verbreitetes, humanes Virus, wobei bei der Primärinfektion, die zumeist im Kindesalter stattfindet, keine Pathogenität induziert wird. Es gibt auch keine Hinweise darauf, daß AAV-2 ein onkogenes Potential besitzen könnte. Aufgrund der hohen Stabilität von

AAV-2 kann das Virus auch aufwendige Reinigungsverfahren ohne Verlust an Infektiösität überstehen.

AAV-2 ist ein kleines, einzelsträngiges DNA-Virus, das zwei Gene trägt: Das rep-Gen kodiert für vier überlappende, regulatorische Proteine, Rep78 und Rep52 und C-terminal gepleißte Varianten der beiden Proteine, Rep68 und Rep40. Die Rep-Proteine dienen zur AAV-Genregulation, DNA-Replikation und Virusverpackung. Das cap-Gen kodiert für die drei Virus-Capsidproteine. Die beiden Gene rep und cap werden von 145 bp langen invertierten Repititionen flankiert, die als "Origins of Replication" dienen. Diese sind die einzigen AAV DNA-Sequenzen, die in Cis für DNA-Replikation, Virusverpackung und Integration in Wirtszellgenom benötigt werden, so daß ca. 4,7 kb lange Fremdsequenzen in die jeweiligen Vektoren kloniert werden können.

AAV sind replikationsdefekt und benötigen für eine effiziente Vermehrung eine Coinfektion mit einem Helfervirus. Ohne Helferviren integriert AAV mit hoher Frequenz ins Wirtszellgenom, wobei ein spezifischer Lokus auf Chromosom 19 (q13.3-qter) stark bevorzugt wird. Die Integration ist dabei unabhängig von der viralen oder zellulären DNA-Replikation. Aufgrund der genannten Vorzüge bieten AAV-Vektoren ideale Voraussetzungen für die Einschleusung und stabile Integration von Genen in nicht prolifierierende Zellen. Für die Gentherapie werden üblicherweise rekombinante AAV-Vektoren eingesetzt, die eine heterologe, für ein gewünschtes Genprodukt kodierende DNA umfassen. Durch die Insertion der heterologen DNA in die AAV-Vektoren wird jedoch die rep und cap-Expression beeinträchtigt. Deshalb müssen zur Vermehrung der rekombinanten AAV-Vektoren diese Proteine bzw. Systeme, die diese Proteine exprimieren, von außen zugeführt werden.

Diese Vermehrung kann beispielsweise durch Cotransfektion von Adenovirus-infizierten Zellen mit dem rekombinanten AAV-Vektor und einem

Helferplasmid erfolgen, im dem die rep- und cap-Gene von AAV durch die Replikationsursprünge ("Origins of Replication") von Adenovirus Typ 5 flankiert werden. Das Helferplasmid wird in den Adenovirus-infizierten Zellen repliziert, so daß ausreichende Mengen an Rep und Cap zur Propagation des AAV-Vektors zur Verfügung stehen. Das rep- und cap-exprimierende Konstrukt weist keine gemeinsamen DNA-Sequenzen mit dem AAV-Vektor auf, so daß kein die Vektorpräparation kontaminierendes Wildtyp AAV durch homologe Rekombination entstehen kann (Samulski et al., J. Virol. 63 (1989), 3822). Ein Nachteil dieses Systems ist jedoch, daß die erreichbaren Virustiter mit 10^4 bis 10^6 infektiösen Partikeln pro ml deutlich niedriger als bei Wildtyp-AAV sind, das bis zu 10^{12} Partikel pro ml erreichen kann. Zudem müssen für jeden Ansatz aufs neue Zellen mit dem AAV-Vektor und dem rep- und cap-exprimierenden Helferplasmid cotransfiziert und anschließend mit Adenovirus infiziert werden, da das Helferplasmid nicht als Virus verpackt wird und somit nicht durch Infektion übertragen werden kann.

J. Conway et al. (J. Virol. 71 (11) (1997), 8780-8789) beschreiben ein Verfahren zur Replikation und Verpackung von rekombinantem AAV Typ 2 mittels eines Herpes Simplex Virus (HSV) Typ 1 Amplikons, das Rep und Cap exprimiert. Die HSV-Amplikons werden in HSV-Hüllen verpackt und können deshalb nur in Gegenwart von Wildtyp-HSV vermehrt werden. Das relative Verhältnis von Wildtyp HSV und verpackten Amplikons ist bei der gemeinsamen Vermehrung nicht vorhersehbar und auch kaum einstellbar. Es gibt auch keine Methode, die beiden Viruspopulationen durch Aufreinigung voneinander zu trennen, da die beiden gemeinsame Hülle die wesentlichen physiko-chemischen Eigenschaften ausmacht. Darüber hinaus besteht das Problem, daß das Amplikon aufgrund von Wachstumsnachteilen bereits nach wenigen Passagen nur noch in einer nicht mehr nachweisbar geringen Menge vorliegt. Das Amplikon-System ist deshalb nur reproduzierbar anwendbar, wenn man für jede rAAV-Präparation das Amplikon-Plasmid transfiziert und dann mit Wildtyp-HSV überinfiziert. Dies hat aber zur Folge, daß man für jede Vermehrungsrunde die Amplikon-

Plasmide erneut transfizieren muß, was aber genau der Nachteil des weiter oben beschriebenen Verpackungssystems ist.

Es wurde versucht, die mit der Verwendung von nicht selbstreplizierenden Plasmiden verbundene Nachteile durch Etablierung von stabilen Zellinien zu lösen, die die AAV-Gene rep und cap in ausreichend hoher Menge exprimieren. Da Rep jedoch toxisch ist, bereitet die Bildung von stabilen Zellklonen, die funktionsfähiges Rep78 oder Rep68 exprimieren, große Schwierigkeiten.

In WO 95/06743 wird ein Verfahren zur Herstellung von rekombinantem AAV beschrieben, bei dem als Helfervirus ein Adenoviruskonstrukt verwendet wird, welches ein die rep- und cap-Gene von AAV aufweisendes rekombinantes Insert umfaßt. Die Expression von Rep-Proteinen in mit AAV infizierten Zellen hemmt jedoch die Adenovirusinfektion, so daß keine hochtitrigen Präparationen erhalten werden können. In WO 95/06743 wird auch die Verwendung eines Herpesvirusvektors anstelle des Adenovirusvektors vorgeschlagen. Allerdings wird keine nacharbeitbare Anleitung gegeben, auf welche Weise stabile rekombinante Herpesviren, die AAV-Genbereiche umfassen, hergestellt werden können, bei denen keine Reversion zum Wildtyp stattfindet.

Eine Aufgabe der Erfindung war es daher, ein System bereitzustellen, mit dem rekombinante AAV-Vektoren als hochtitrige Präprationen, wie sie für Anwendungen im klinischen Maßstab benötigt werden, hergestellt werden können. Eine weitere Aufgabe der Erfindung war es, ein Helferkonstrukt zur Vermehrung von AAV-Vektoren bereitzustellen, bei dem die Nachteile des Standes der Technik mindestens teilweise beseitigt sind.

Diese Aufgaben werden erfindungsgemäß durch stabile Zellinien gelöst, die die AAV-Gene rep und cap in ausreichend hoher Menge exprimieren, und in denen AAV-Vektoren durch Infektion propagiert werden können.

Die Erfindung betrifft ein rekombinantes Herpesvirus, welches dadurch gekennzeichnet ist, daß es ein rep- und ein cap-Gen von Adeno-assoziierten Viren (AAV), beispielsweise ein rep- und ein cap-Gen von AAV-2 oder ein damit funktionell äquivalentes Gen, in operativer Verknüpfung mit einer Expressionskontrollsequenz enthält. Vorzugsweise befinden sich das rep- und cap- Gen auf einer Insertion, die im Genom das Herpesvirus an einer geeigneten Stelle integriert ist.

Das erfindungsgemäße rekombinante Herpesvirus enthält zum einen die für die effiziente Vermehrung von AAV benötigten Helferfunktionen und kann daneben die für Rep und Cap kodierenden Bereiche von AAV in ausreichender Menge exprimieren, so daß eine Vermehrung und Verpackung von AAV-Vektoren in Zellkultur bei Coinfektion mit dem rekombinanten HSV (rHSV) möglich ist.

Als Expressionskontrollsequenzen sind alle Sequenzen geeignet, die zu einer ausreichenden Expression von rep und cap in der Zielzelle führen, beispielsweise homologe AAV-Expressionskontrollsequenzen, wie etwa der AAV p5 Promotor, oder heterologer Promotoren, z.B. eukaryontische zelluläre oder virale Promotoren. Es können konstitutive oder regulierbare Expressionskontrollsequenzen verwendet werden. Das rep- und das cap-Gen können unter gemeinsamer Kontrolle einer einzigen Expressionskontrollsequenz oder jeweils unter Kontrolle einer separaten - gleichen oder verschiedenen - Expressionskontrollsequenz stehen.

Überraschenderweise wurde festgestellt, daß Herpesviren, insbesondere HSV, gegenüber einer hohen Expression der AAV-Rep-Proteine resistent sind. Durch Integration des rep- und des cap- Gens in ein Herpesvirus, welches ohnehin als Helfervirus für die Vermehrung der Helfervirus-abhängigen AAV-Vektoren erforderlich ist, konnte ein Konstrukt erhalten werden, welches alle zur AAV-Vermehrung benötigten Funktionen aufweist und eine Herstellung der für die Vektorpropagation benötigten AAV-Proteine

in großen Mengen ermöglicht. Mit einem solchen System können infektiöse AAV-Vektoren in großem Maßstab hergestellt werden, wie sie für die Gentherapie im klinischen Maßstab benötigt werden. Die Bildung von rekombinanten AAV ist somit nicht mehr, wie bei der Verwendung von Plasmiden, von Transfektionseffizienzen abhängig.

Das erfindungsgemäße Herpesvirus ist genetisch stabil und zeigt bevorzugt keine Reversion zum Wildtyp. So findet man auch nach mehreren aufeinander folgenden Verdünnungsschritten bei einer Plaque-Reinigung, z.B. nach 3, bevorzugt nach 5 und besonders bevorzugt nach 7 Verdünnungsschritten keine sichtbare Reversion zum Wildtyp, was zeigt, daß die integrierte Kassette stabil bleibt. Ein weiterer Vorteil des erfindungsgemäßen Herpesvirus ist, daß es mit einem hohen Titer kultiviert werden kann, z.B. mit einem Titer von $\geq$ 5%, insbesondere $\geq$ 10% und besonders bevorzugt $\geq$ 20% des Titers des entsprechenden Herpesvirus-Wildtyps, wobei der Titer dabei bevorzugt als Cell-Release-Virus (CRV)-Titer bestimmt wird.

Das erfindungsgemäße rekombinante Herpesvirus enthält weiterhin bevorzugt ein Reportergen, dessen Exprimierbarkeit in Assoziation mit der Integration des rep- und des cap-Gens steht. Das Reportergen steht in operativer Verknüpfung mit einer geeigneten Expressionskontrollsequenz, wie etwa einem SV40-Promotor oder einem anderen Promotor, z.B. einem HSV- oder AAV-Promotor. Bevorzugt ist das Reportergen ein Nichtantibiotikumresistenz-Gen, besonders bevorzugt ein für ein direkt, z. B. visuell nachweisbares Polypeptid, z.B. LacZ oder GFP (Green Fluorescence Protein) kodierendes Gen. Durch Expression des Reportergens kann die Reinheit von AAV-Präparationen, die das rekombinante Herpesvirus nicht mehr enthalten dürfen, überwacht werden. Weiterhin wird auch eine Kontrolle der Reinheit von rekombinanten Herpesviruspräparationen gegenüber Verunreinigungen mit Wildtyp-Herpesviren ermöglicht.

Grundsätzlich kann jedes Mitglied der Herpesvirusfamilie (Herpesviridae) durch Insertion eines rep- und eines cap-Gens von AAV in ein erfindungsgemäßes rekombinantes Herpesvirus überführt werden. Beispiele geeigneter Herpesviren sind das Herpes-Simplex-Virus (HSV), das Cytomegalovirus (CMV), das Pseudorabiesvirus (PRV) und das Epstein-Barrvirus (EBV). Besonders bevorzugt ist das Herpes-Simplex-Virus (HSV) und insbesondere HSV-Typ I. Günstigerweise wird ein Herpesvirus verwendet, welches eine singuläre Restriktionsstelle aufweist, z. B. die HSV-Typ I Mutante 1802 (Rixon et al., J. Gen. Virol.71 (1990), 2934-2939), welche nur eine einzige XbaI-Stelle in der U_S-Region an Position 143 969 (die Nummerierung der Positionen erfolgt gemäß McGeoch et al., Nucl. Acids Res. 14 (1986), 1727-1745) aufweist.

Das Herpesvirus kann das rep- und das cap-Gen von AAV in einer nichtessentiellen Region enthalten, z.B. in der U_S- oder/und U_L- Region. Bevorzugt ist auch die Verwendung replikationsdefizienter Herpesvirusmutanten. Hierzu kann man das rep- oder/und das cap-Gen in einen Bereich des Herpesvirusgenoms inserieren, der für die Replikation des Herpesvirus benötigt wird, nicht aber für die AAV-Replikation. Alternativ kann eine Herpesvirus-Mutante verwendet werden, in der schon von vorneherein das entsprechende Herpesvirus-Replikationsgen deletiert ist. In Frage kommt beispielsweise das UL9-Gen, das für die HSV-Replikation absolut essentiell, aber für die AAV-Replikation überflüssig ist (Weindler et al., J. Virol. 65 (1991), 2476-2483). Darüber hinaus ist auch das UL54-Gen geeignet, das für das Immediate Early Protein ICP27 kodiert. Auch dieses Gen wird nicht für die AAV-Replikation benötigt. Die Deletion des UL54-Gens führt zu einer Verlangsamung des Herpesvirus-Replikationszyklus, die entsprechende Mutante ist aber jedoch nicht komplett replikationsdefizient, im Gegensatz zu einer Mutation im UL9-Gen. Darüber hinaus kommen auch noch andere Herpesvirus-Gene für die Insertion in Frage, deren Mutation oder/und Deletion den gleichen Effekt hat, nämlich eine Verlangsamung bzw. eine vollständige Blockierung des Herpesvirus-Replikationszyklus.

Bevorzugt umfaßt das rekombinante Herpesvirus nicht die vollständige invertierte Repetitionsequenz (ITR) von AAV und besonders bevorzugt ist es vollständig frei von Anteilen der ITR-Sequenz von AAV.

Eine zusätzliche Verbesserung kann durch Verwendung regulierbarer Expressionskontrollsequenzen für das rep- oder/und das cap-Gen, insbesondere für das rep-Gen erzielt werden. Beispiele hierfür sind Expressionskontrollsequenzen, die durch Zugabe von Tetracyclin (Gossen und Bujard, Proc. Natl. Sci. USA (1992), 5547-5551) oder durch Zugabe von Ecdyson (No et al., Proc. Natl. Acad. Sci. USA (1996), 3346-3351) regulierbar sind. Alternativ können auch Promotoren verwendet werden, die die Expression von "early" und "late" Herpesvirusproteinen, z.B. von HSV steuern.

Ein weiterer Gegenstand der Erfindung ist ein Verfahren zur Herstellung eines rekombinanten Herpesvirus, wobei man das rep- und das cap-Gen von AAV in das Genom eines Herpesvirus stabil integriert. Dazu wird die Herpesvirus-DNA bevorzugt an einer oder mehreren gewünschten Stellen gespalten und ein das rep- und das cap-Gen enthaltendes DNA-Fragment, z.B. ein Plasmid,in die Herpesvirus-DNA ligiert. Die Spaltung wird bevorzugt mit Restriktionsenzymen, beispielsweise mit Xbal,durchgeführt. Alternativ können die rep- und cap-Gene auch durch homologe Rekombination in das Herpesvirusgenom inseriert werden. Das rep-cap-Konstrukt muß dann flankierende Sequenzen aufweisen, die mit der für die Insertion ins Herpesvirusgenom vorgesehenen DNA-Sequenz übereinstimmen oder zumindest eine hohe Homologie aufweisen.

Ein weiterer Gegenstand der Erfindung ist eine Nukleinsäure, die aus einem erfindungsgemäßen rekombinanten Herpesvirus stammt und das rep- und das cap-Gen von Adeno-assoziierten Viren (AAV) sowie die von einem Herpesvirus stammenden, zur Vermehrung von rekombinanten Adeno-assoziierten Virusvektoren benötigten Helferfunktionen jeweils in operativer

Verknüpfung mit Expressionskontrollsequenzen enthält. Diese Nukleinsäure befindet sich vorzugsweise auf einem Vektor, insbesondere auf einem eukaryontischen Vektor.

Die Erfindung umfaßt weiterhin eine Viren-Zusammensetzung, die den erfindungsgemäßen rekombinanten Herpesvirus enthält. Eine solche Zusammensetzung ist insbesondere dadurch gekennzeichnet, daß sie frei von Wildtyp-Herpesvirus ist.

Unter dem Begriff Virus, wie er hierin verwendet wird, sind auch Virionen zu verstehen.

Die erfindungsgemäßen rekombinanten Herpesviren und Vektoren werden vorteilhaft zur Herstellung von hochtitrigen, infektiösen rAAV-Vektorpräparationen verwendet. Deshalb umfaßt die Erfindung ein Verfahren zur Herstellung infektiöser AAV-Vektorpräparationen, welches die Schritte umfaßt:

(a) Bereitstellen eines viralen Vektors auf der Basis von Adeno-assoziierten Viren (AAV), welcher eine heterologe DNA-Insertion umfaßt,

(b) Bereitstellen eines rekombinanten Herpesvirus, das ein rep- und ein cap-Gen von AAV in operativer Verknüpfung mit einer Expressionskontrollsequenz enthält,

(c) Einbringen des AAV-Vektors aus (a) und des rekombinanten Herpesvirus aus (b) in eine Zelle, z.B. durch Infektion, oder/und DNA-Transfektion,

(d) Vermehren des AAV-Vektors und

(e) Gewinnen einer infektiösen AAV-Vektorpräparation.

Anstelle des rekombinanten Herpesvirus (bzw. Virions) kann auch ein entsprechender Vektor, welcher das rep- und das cap-Gen von AAV sowie

die zur Replikation und Verpackung von AAV notwendigen Helfer-funktionen enthält, eingesetzt werden.

Bevorzugt wird die Zelle mit dem rekombinanten AAV-Vektor transfiziert oder infiziert und anschließend mit dem rekombinanten Herpesvirus infiziert. Besonders bevorzugt werden sowohl der AAV-Vektor als auch das Herpesvirus durch Infektion in die Zelle eingebracht, da auf diese Weise das Auftreten einer unerwünschten illegitimen Rekombination weitestgehend unterdrückt werden kann. Für das erfindungsgemäße Verfahren kann ein replizierbares rekombinantes Herpesvirus verwendet werden. Bevorzugt wird jedoch ein nicht oder nur eingeschränkt replizierbares rekombinantes Herpesvirus eingesetzt, was zu einer weiteren Erhöhung der Ausbeute an AAV führt. Mit dem erfindungsgemäßen Verfahren ist es möglich, hochtitrige, infektiöse AAV Vektorpräparationen, insbesondere eingekapselte rAAV-Präparationen zu gewinnen.

Mit Hilfe des erfindungsgemäßen rekombinanten Herpesvirus (Virions) oder Vektors, die die zur AAV-Vermehrung benötigten Helferfunktionen umfassen sowie eine ausreichende Menge von Rep und Cap Proteinen bereitstellen, können AAV-Vektoren durch Infektion von eukaryontischen Zellen einschließlich verschiedener, allgemein verfügbarer Zellinien vermehrt werden. Ein weiterer Gegenstand der Erfindung ist deshalb eine Zelle, die einen erfindungsgemäßen rekombinanten Herpesvirus oder Vektor enthält. Die Zelle ist vorzugsweise eine Säugerzelle, insbesondere eine permanent kultivierbare Zelle. Beispiele sind Nagerzellen wie BHK-Zellen, z.B. BHK21. Es können aber auch andere Zellen, z.B. humane Zellen wie etwa Vero- oder HeLa-Zellen verwendet werden.

Die Zelle kann das Virus, den Vektor oder das Virion in extrachromosomaler Form in einer oder mehreren Kopien enthalten. Derartige Zellen sind beispielsweise durch Infektion erhältlich. Alternativ kann das Virus, der

Vektor oder das Virion auch im Genom der Zelle integriert vorliegen. Bevorzugt wird die Zelle durch Infektion mit dem Virus erzeugt.

Darüber hinaus kann die Zelle weiterhin einen rekombinanten AAV-Vektor, insbesondere einen AAV-Vektor mit einer heterologe DNA-Insertion, der für therapeutisch wirksames Polypeptid kodiert, enthalten. Der AAV-Vektor kann extrachromosomal oder integriert im Genom der Zelle latent vorliegen. Er wird dann bei Infektion mit rekombinantem Herpesvirus freigesetzt und repliziert dann wie nach einer AAV-Vektor-Infektion.

Die Infektion von Säugerzellen mit dem erfindungsgemäßen rekombinanten Herpesvirus ergab eine hohe Expression der rep- und cap-Gene, wobei die Ausbeuten einer Coinfektion mit AAV-Wildtyp und einem Herpes-Simplex Virus vergleichbar waren.

Schließlich betrifft die Erfindung noch ein verbessertes Verfahren zur Herstellung von infektiösen AAV-Vektorpräparationen, bei dem gegenüber bekannten Verfahren, bei denen der AAV-Vektor durch Transfektion in eine Wirtszelle eingebracht wurde, eine signifikante Verringerung des Auftretens unerwünschter illegitimer Rekombinationen gefunden wird. Das Verfahren umfaßt das Einbringen eines AAV-Vektors und eines beliebigen Helfervirus, z.B. eines Adenovirus, eines Herpesvirus und insbesondere eines erfindungsgemäßen rep/cap exprimierenden Herpesvirus, in eine Zelle, die Kultivierung der Zelle unter geeigneten Bedingungen zur Vermehrung des AAV-Vektors und das Gewinnen einer infektiösen AAV-Vektorpräparation aus der Zelle oder/und dem Kulturüberstand, wobei das Verfahren dadurch gekennzeichnet ist, daß der AAV-Vektor und das Helfervirus beide durch Infektion in die Zelle eingebracht werden.

Die Erfindung wird durch die beigefügten Figuren und die folgenden Beispiele weiter erläutert.

Figur 1 zeigt die Genomstruktur eines erfindungsgemäßen rHSV/AAV. Die Position 143 969 der Xbal-Stelle in HSV-1 1802 ist gemäß der Nummerierung von McGeoch et al., Nucl. Acids Res. Nr. 14 (1986), 1727-1745). Die Nummerierung des AAV-Genoms erfolgt gemäß der Genbankhinterlegungsnummer J01901.

Figur 2 zeigt die Expression von AAV-Rep-Proteinen kurz (A) oder lange (B) nach einer Infektion von BHK-Zellen mit rHSV/AAV.

Figur 3 zeigt die Expression von AAV-Cap-Proteinen kurz (A) oder lange (B) nach einer Infektion von BHK-Zellen rHSV/AAV.

Figur 4 zeigt die Lokalisierung von Rep oder Cap Proteinen und assemblierten AAV Capsiden in rHSV/AAV-infizierten BHK-Zellen durch Immunofluoreszenz.

Figur 5 zeigt das Ergebnis eines Replikationscenterassays, in dem das herkömmliche und das erfindungsgemäße Verfahren verglichen werden.

Figur 6 zeigt das Ergebnis eines infektiösen Titerassays von rAAV/GFP in Rohlysaten.

Beispiele

1. Material und Methoden

1.1 Kultivierung von Zellen

BHK-21-Zellen (Stoker et al., Nature, 203 (1964), 1355-1357; ECACC Nr. 8501143) wurden als Monoschicht in G-MEM (Gibco BRL Nr. 21710-025) mit 10% NCS: (Newborn Calf Serum) (Gibco BRL-Nr. 16010-084), 1 x Tryptosephosphat-Bouillon (Gibco BRL-Nr. 18060-02) und Pen/Strep (Seromed) bei 37°C, 5% CO_2 gezüchtet. Um BHK-Zellen in Rollerflaschen (Falcon 850 cm^3, Nr. 3027) zu kultivieren, wurde ein Volumen von 50 ml Medium verwendet und die Flaschen wurden mit 0,8 U/min bei 37°C, 5% CO_2 gedreht. Zur Infektion von in den Rollerflaschen wachsenden BHK-21-Zellen wurde das Volumen auf 15 ml komplettes G-MEM reduziert. BHK-21-Zellen wurden bis zu 15 Passagen vor dem Beginn einer neuen Kultur kultiviert.

HeLa- und Vero-Zellen wurden in D-MEM (Gibco Nr. 21855-025) mit 10% FCS (Seromede Nr. S0115) und Pen/Strep (Seromed) gezüchtet.

1.2 Herstellung von infektiösen HSV und rHSV Präparationen

Wildtyp- oder rekombinante Herpes Simplex Viren (HSV) wurden durch Infektion von etwa 2 x 10^8 BHK-21-Zellen, die in Rollerflaschen wie in Beispiel 1 beschrieben, gezüchtet wurden, in einer Multiplizität der Infektion (MOI) von 0,002 vermehrt. Der Infektionsverlauf wurde durch die Zunahme des cytopathischen Effekts (CPE) in der Zellkultur überwacht. 3 Tage nach der Infektion zeigten die meisten Zellen einen vollständigen CPE und konnten durch Schütteln im Zellkulturmedium gesammelt werden.

Nach Zentrifugation bei 1500 x g für 10 min bei 4°C wurde Virus aus zellfreiem Überstand (CRV; Cell-Released-Virus) gewonnen, in Aliqots aufgeteilt und bei -80°C eingefroren.

Das Zellpellet wurde in PBS (Phosphat-gepufferte Salzlösung) resuspendiert und für 1 min bei 4°C beschallt. Nach Zentrifugation mit 2000 x g für 10 min bei 4°C) wurde der Überstand als zellassoziiertes Virus (CAV) gewonnen, in Aliquots aufgeteilt und bei -80°C eingefroren.

1.3 Reinigung von HSV-Virionen

Zur Herstellung von HSV-Virionen wurden in Rollerflaschen kultivierte BHK-Zellen wie in 1.2 beschrieben infiziert. Nach Zentrifugation wurde der CRV-enthaltende klare Überstand in Zentrifugationsröhrchen überführt. Virionen wurden durch Zentrifugation für 2 h bei 4°C mit 23 000 x g pelletiert, was 13 500 U/min bei Verwendung eines Beckman SW28-Rotors entspricht. Das Viruspellet wurde in 1 ml MEM ohne Phenolrot (MEM-PR) resuspendiert und durch Beschallung bei 4°C (3 x für 30 sec) homogenisiert. Die Suspension wurde auf einen linearen Ficollgradienten (5% + 15% w/v in MEM-PR) in Beckman SW28 Ultraclear Röhrchen geschichtet und für 2 h bei 4°C mit 12 000 U/min (19 000 x g) zentrifugiert.

Bei Beleuchtung war die konzentrierte Virionen-Bande in der Mitte des Röhrchens sichtbar. Oberhalb der Virionen-Bande kann eine diffuse Bande sichtbar sein, welche beschädigte Partikel enthält. Die Virionen-Bande wurde durch Punktieren des Röhrchens mit einer 21 oder 23 Gauge-Nadel gesammelt, in ein neues Beckman SW28 Ultraclear Röhrchen überführt und mit MEM-PR auf ein Endvolumen von 35 ml verdünnt. Dann wurden die Virionen durch Zentrifugation für 2 h bei 4°C mit 22 200 U/min (65 000 x g) pelletiert. Das Pellet wurde in MEM-PR resuspendiert und bei -80°C gelagert. Zur Herstellung von viraler DNA wurde das Pellet in 300 µl TE-

Puffer resuspendiert und in ein 1,5 ml Röhrchen zur weiteren Verarbeitung überführt.

Alternativ wurden HSV-Virionen unter Verwendung eines CsCl-Gradienten aufgereinigt.

1.4. Herstellung von HSV-DNA

Dem gemäß 1.3 gewonnenen, in 300 µl TE resuspendierten Virionpellet wurden SDS (Endkonzentration von 0,2 %) und Proteinase K (Endkonzentration 300 µg/ml) zugegeben. Der Ansatz wurde für mindestens 1 h bei 37°C inkubiert. Nach Zugabe von Natriumacetat pH 9,2, auf eine Endkonzentration von 0,3 M und einer Phenol/Chloroform-Extraktion (2 x Phenol/CIA (Chloroform-Isoamylalkohol), 1 x CIA), wurde die DNA durch Zentrifugation nach Zugabe von 2 Volumina Ethanol präzipitiert. Das Pellet wurde mit 70% Ethanol gewaschen, getrocknet und in TE (Tris-EDTA-Puffer, 10 mM Tris HCl, 1 mM EDTA) resuspendiert.

1.5 Herstellung des Plasmids psub201lac

Das auf pCH110 (Pharmacia) basierende Plasmid pFJ3, welches ein lacZ-Gen unter der Kontrolle eines SV40 Promotors enthält (Rixon et al., J. Gen. Virol. 71 (1990) 2931-2939), wurde mit BamHI gespalten und dephosphoryliert. Das XbaI-Fragment von psub201 (Samulski et al., J. Virol. 61 (1987), 3096-3101), das die Sequenz 191-4485 des Adeno-assoziierten Virus Typ 2 (Genbank Zugangs-Nr. J019901) einschließlich der rep- und der cap-Gene und der Promotoren p5, p19 und p40 aber ohne die Sequenzen der invertierten terminalen Repetitionen (ITR) enthält, wurde in pFJ3 insertiert, um psub201lac zu ergeben.

1.6 Plaqueassay

Subkonfluente BHK-21 Zellen wurden mit verschiedenen Verdünnungen von HSV CRV oder CAV Präparationen infiziert. Nach 1 h Adsorption bei 37°C wurden die Zellen mit PBS gewaschen und mit G-MEM enthaltend 0,5% Sea Plaque-Agar, 5% NCS, Pen/Strep und 1 x Tryptose-Phosphat-Bouillon überschichtet. Nach Inkubation für 3 Tage bei 37°C, 5% CO_2 wurden die Plaques gezählt und der Titer bestimmt.

1.7 X-Gal-Anfärbung

Infizierte oder nichtinfizierte Zellen wurden 1 x mit 150 mM NaCl, 15 mM Natriumphosphat, pH 7,3 in PBS gespült. Die Zellen wurden durch Inkubation für 5 min in kaltem PBS, enthaltend 2 % Formaldehyd und 0,2 % Glutaraldehyd fixiert. Um das Fixativ zu enfernen, wurden Zellen mit PBS gewaschen. Schließlich wurden die Zellen mit der X-Gal-Anfärbelösung enthaltend 1 mg/ml X-Gal, 5 mM Kaliumferrocyanid, 5 mM Kaliumferricyanid, 2 mM $MgCl_2$ in PBS überschichtet. Angefärbte Zellen wurden üblicherweise für mehrere Stunden bei 37°C inkubiert, bis eine blaue Färbung sichtbar war.

1.8 Westernblot

Der Westernblot wurde, wie beim Laemmli, Nature, 227 (1970) 680-685 beschrieben, durchgeführt. Die Zellen wurden 2 x mit PBS gewaschen, entweder während sie noch an die Platte anhafteten oder nachdem sie gesammelt und in einem 15 ml Röhrchen pelletiert waren. Nach Zugabe von 100 µl 1 x SDS Probenpuffer (50 mM Tris-Cl, pH 6,8; 1% ß-Mercaptoethanol; 2% SDS; 0,1 % Bromphenolblau; 10% Glycerin) pro 1 x 10^5 Zellen wurde die Suspension in ein 1,5 ml Reaktionsgefäß überführt. Die Proben wurden in kochendem Wasser für 10 min inkubiert, auf Eis gekühlt und bei -80°C gelagert. Zur Analyse wurden bis zu 30 µl jeder Probe auf ein

10% SDS Polyacrylamidgel (SDS-PAGE) gegeben. Nach der Elektrophorese wurde das Gel 15 min in einer Tris-Glycinlösung (25 mM Tris-Base; 95% mM Glycin; 10% Methanol) äquilibriert. Die Proteine wurden unter Verwendung einer halbtrockenen Blotvorrichtung und 1 mA/cm² auf eine Nitrozellulosemembran (Schleicher und Schuell, BA85, Nr. 401196) transferiert. Zur Kontrolle des Transfers und der Proteinmenge wurde die Membran mit Ponceau-S (Sigma) angefärbt. Die Membran wurde in PBS, 0,3% Tween-20, 10% fettfreiem Milchpulver für 30 min bei Raumtemperatur oder über Nacht bei 4°C blockiert.

Antikörper wurden entsprechend in PBS, 0,3% Tween-20, 10% fettfreies Milchpulver verdünnt und für mindestens 1 h bei Raumtemperatur oder über Nacht bei 4°C inkubiert. Zur Rep-Detektion wurden die monoklonalen Antikörper 303.9 und 76.3 (1:10 verdünnt) verwendet (Kleinschmidt et al. Virology 206 (1995) 254-262; Wistuba et al., J. Virol. 69 (1995), 5311-5319). Zur Detektion der Cap (VP)-Proteine wurde der Antikörper B1 (1:10 verdünnt) verwendet (Wistuba et al. (1995) supra). Die Filter wurden dreimal für 10 min mit PBS, 0,3% Tween-20 bei Raumtemperatur gewaschen. Zur Detektion von AAV-Capsidstrukturen wurde der Antikörper A20 (Wistuba et al., J. Virol. 71 (1996), 1341-1352) verwendet.

Der zweite Antikörper, üblicherweise ein Anti-Maus-Antikörper-Peroxidase-Konjugat, wurde in PBS, 0,3% Tween-20, 10% fettfreiem Milchpulver verdünnt und zusammen mit dem Filter für 30 min bis 1 h bei Raumtemperatur inkubiert. Die detektierten Proteine wurden über einen ECL-Kit gemäß Angaben des Herstellers (Amersham Life Science, RPN 2106) sichtbar gemacht.

1.9 Immunofluoreszenz

Zellen wurden auf Deckgläsern gezüchtet und mit HSV oder rHSV in einer MOI von 1 infiziert. 24 h nach Infektion wurden die Deckgläser 3 x mit PBS

(Phosphat gepufferte Salzlösung) gewaschen, 5 min in eisgekühltem Methanol inkubiert und wiederum mit PBS gewaschen. Zum Blocken wurden die Deckgläser 30 min in PBS mit 10% NCS inkubiert. Dann erfolgte eine Inkubation für 1 h in einer Feuchtkammer mit den jeweiligen Detekions-Antikörpern (siehe 1.8), welche üblicherweise 1:1 in PBS mit 10% NCS verdünnt waren. Nach dreimaligem Waschen mit PBS wurden die Deckgläser für weitere 30 min mit verdünntem Fluorescein-Isothiocyanat (FITC) markiertem Anti-Mausantikörper inkubiert. Nach drei weiteren Waschschritten mit PBS wurden die Deckgläser mit einem Fluoreszenzmikroskop analysiert.

1.10 Herstellung von rAAV

Für die Herstellung von rAAV Vektoren wurde das herkömmliche Verfahren (Cotransfektion) sowie das erfindungsgemäße rHSV/AAV-System verwendet. Die Experimente wurden mit BHK-21 Zellen durchgeführt, die entweder mit Wildtyp HSV Typ 1 Stamm 1802 oder mit dem erfindungsgemäßen rHSV/AAV infiziert wurden. Es wurde ein rAAV-GFP-(UF5) verwendet, der das Reporterprotein GFP (Green Fluorescence Protein) exprimiert (Zolotukhin et al., J. Virol. 70 (1996), 4646-4654). Die Plasmidpräparationen, die das rAAV Genom flankiert von den terminalen Repetitionseinheiten enthielten, wurden auf ihre Integrität hinsichtlich der terminalen Repetitionen überprüft, bevor sie in den Experimenten verwendet wurden.

BHK-21 Zellen, gezüchtet auf 5,5 cm Platten, wurden für das herkömmliche Verfahren mit 10 µg rAAV-GFP (UF5) Plasmid DNA und 10 µg ΔTR DNA (rep/cap-exprimierendes Plasmid) oder für das erfindungsgemäße Verfahren nur mit 10 µg rAAV-GFP (UF5) DNA transfiziert. Nach Inkubation über Nacht bei 37°C, 5% CO_2 wurden die Zellen zweimal mit serumfreien G-MEM und einmal mit PBS gewaschen, bevor komplettes G-MEM Medium zugegeben wurde. Dann wurden die Zellen 6 bis 12 h lang entweder mit

wtHSV-1 1802 in einer MOI von 1 (herkömmliches Verfahren) oder rHSV/AAV in MOIs von 0,01 bis 1 (erfindungsgemäßes Verfahren) infiziert. Nach Adsorption für eine Stunde bei 37°C wurden die Zellen einmal mit PBS gewaschen und komplettes G-MEM wurde zugegeben. Die infizierten Zellen wurden bei 37°C, 5% CO_2, bis zu einem vollständigen CPE (üblicherweise 2 bis 3 Tage) inkubiert. Zur Ernte wurden die Platten bei -80°C eingefroren und nach Auftauen wurden die Zellen in ein 15 ml Röhrchen überführt. Nach zwei weiteren Gefrierzyklen in flüssigem Stickstoff und Auftauen wurden die zellulären Trümmer durch Zentrifugation für 15 min bei 4°C mit 1500 x g entfernt. Der klare Überstand wurde als Rohlysat gesammelt und das Helfervirus wurde durch Inkubation bei 56°C für 15 bis 30 min inaktiviert. Das Lysat wurde direkt analysiert oder weiter auf einem CsCl-Gradienten gereinigt.

1.11 Bestimmung der Anzahl an physikalischen rAAV Partikeln

Die Anzahl an physikalischen rAAV-Partikeln wurde durch eine Dot Blot-Analyse bestimmt. Zu 5 µl der rAAV enthaltenden Probe, erhalten aus einer CsCl-Gradientenfraktion oder einem Rohlysat, wurden 20 µl 10 x DNase I-Reaktionspuffer (500 mM Tris-Cl, pH 7,5; 100 mM $MgCl_2$; 500 µg/ml BSA), 5 µl DNase I (12 U) und 170 µl H_2O zugegeben. Nach Inkubation bei 37°C für 1 h wurden 200 µl 2 x Proteinase K-Puffer (20 mM Tris-Cl, pH 8,0, 20 mM EDTA, pH 8,0, 1% SDS) und 100 µg Proteinase K zugegeben. Nach einer weiteren Inkubation für 1 h bei 37°C wurde ein 1/10 Volumen 3 M Natriumacetat (pH 9,2) zugegeben und die Proben wurden einer Phenolextraktion (1 x Phenol, 1 Phenol/CIA, 1 x CIA) unterzogen. Nach Zugabe von 40 µg Glykogen und 2,5 Volumen 100% Ethanol wurde 30 min bei -80°C inkubiert. Schließlich wurde die DNA durch Zentrifugation für 30 min bei maximaler Geschindigkeit pelletiert. Die Pellets wurden einmal mit 70% Ethanol gewaschen, getrocknet und schließlich in 400 µl 0,4 M NaOH, 10 mM EDTA-Lösung resuspendiert.

Als Standard wurden zweifache serielle Verdünnungen von rAAV Vektor DNA (40 bis 0,3 125 ng Plasmid) in einem Volumen von 20 µl hergestellt und mit 0,4 NaOH, 10 mM EDTA-Lösung versetzt. Alle Proben wurden 5 Minuten bei 100 °C inkubiert und sofort auf Eis gekühlt. Unter Verwendung einer Dot Blot-Vorrichtung wurden die Proben auf Gene Screen-Plus Membranen (NEN Light Science Products) überführt und die DNA wurde auf den Filtern durch UV-Licht vernetzt. Die Hybridisierung wurde gemäß Church et al., supra, bei 65°C in 0,25 M Natriumphosphatpuffer, pH 7,2, 1 mM EDTA, 7 % SDS und 1% BSA durchgeführt. Nach 30 min bis 2 h einer Vorhybridisierung wurden die Membranen über Nacht an das [α-^{32}P]dCTP-markierte 731 bp NotI-Fragment von rAAV-GFP hybridisiert. Die Filter wurden bei 65°C dreimal mit Waschpuffer I (20 mM Natriumphosphatpuffer, pH 7,2; 2,5% SDS; 0,25% BSA; 1 mM EDTA) und weitere dreimal mit Waschpuffer II (20 mM Natriumphosphatpuffer, pH, 7,2; 1% SDS, 1 mM EDTA) gewaschen. Nach Exposition der Filter auf Röntgenfilme wurden die Flecken ausgeschnitten und in einem Szintillationszähler analysiert. Die Anzahl an physikalischen Partikeln wurde unter Verwendung der doppelsträngigen rAAV-Plasmid DNA als Standard berechnet.

1.12 Bestimmung des infektiösen Titers von rAAV-Präparationen durch einen den Replikationscenterassay

Zur Durchführung eines Replikationscenterassays wurden die Zellen geerntet, bevor rAAV aus der primär infizierten Zelle freigesetzt ist und eine Sekundärinfektion sich in der Kultur verbreitet. Etwa 5 x 10^4 HeLa-Zellen wurden pro Vertiefung auf eine 12-Well-Platte gegeben. Nach Inkubation über Nacht wurden die Zellen entweder mit Adenovirus (MOI = 20) alleine um wtAAV nachzuweisen oder mit Adenovirus (MOI = 20) und wtAAV (MOI = 4) um rAAV nachzuweisen, infiziert. Nach 1 h Adsorption wurden die Zellen gewaschen und mit 100 µl rAAV-GFP enthaltendem Lysat infiziert. Nach 1 h wurde ein 1 ml frisches Medium zugegeben. Dann wurden die

Zellen bei 37°C, 5% CO_2 für 24 h inkubiert und durch Zentrifugation pelletiert. Noch haftende Zellen wurden trypsiniert und mit den pelletierten Zellen vereinigt. Die Zellen wurden resuspendiert und unter Verwendung einer Vakuumvorrichtung auf Nitrozellulosefilter übertragen. Die Hybridisierung der Nitrozellulosefilter wurde in einer Formamidlösung (5 x SSC; 50 % Formamid; 5 x Denhardt; 50 mM Natriumphosphatpuffer, pH 7,2; 0,1 % SDS; 0,1 mg/ml Hefe tRNA) bei 42°C entweder mit dem [α-^{32}P]dCTP-markiertem 731 bp NotI-Fragment von rAAV-GFP oder dem [α-^{32}P]dCTP-markierten 1465 bp-Fragment von AAV rep durchgeführt.

2. Ergebnisse

2.1 Herstellung von rekombinantem HSV/AAV

Als Ausgangsmaterial wurde die HSV-Typ I Mutante 1082 (Rixon et al., J. Gen. Virol. 71 (1990) 2931-2939) verwendet, die nur eine einzige XbaI-Stelle in der U_s-Region an Position 143 969 (Nummerierung gemäß McGeoch et al., supra) enthält. Diese Position ist zur Integration von heterologen Sequenzen geeignet, da zum einen keine offenen Leserahmen beeinflußt werden und zum anderen keines der 5 in diesem Bereich befindlichen Gene zur Virusvermehrung in Zellkultur essentiell ist. Die Vorgehensweise zur Herstellung von rHSV ist in Abb. 1 gezeigt.

psub201lac wurde mit XbaI gespalten, um die vollständige 8,4 kb lange Expressionskassette auszuschneiden. Anschließend wurde die gelgereinigte Expressionskassette in die XbaI-Stelle von HSV-1 1802 ligiert. Dazu wurde HSV DNA vollständig mit Xba gespalten. 1 μg der XbaI-gespaltenen HSV DNA wurde mit 1 μg gereinigtem XbaI-Fragment von psub201lac in einem Volumen von 20 μl ligiert. Der ligierte HSV 1802/psub201lac wurde dann in BHK-21 Zellen unter Verwendung des folgenden Verfahrens transfiziert. 1 ml HBS, 1 μl Heringsperma DNA (10 μg/μl) und 10 μg ligierter HSV 1802/psub201lac (1 μg) wurden vermischt. Anschließend wurden 70 μl 2

M $CaCl_2$ tropfenweise zugegeben. Die Lösung wurde nach Entfernen des Wachstumsmediums auf BHK-Zellen gegossen. Nach Inkubation für 40 min bei 37°C wurden 4 ml komplettes G-MEM (mit 5% NCS) zugegeben und die Zellen für weitere 200 min inkubiert. Nach Entfernen des Mediums wurden die Zellen 1 mal mit Serumfreiem G-MEM gewaschen. Die transfizierten Zellen wurden dann mit 1 ml 20 % DMSO in HBS für 4 min bei Raumtemperatur behandelt. Die DMSO-Lösung wurde entfernt und die Zellen wiederum mit serumfreiem G-MEM gewaschen. Nach Zugabe von G-MEM mit 5% NCS wurden die Zellen 3 Tage gezüchtet, bis Plaques sichtbar waren und das Virus geerntet wurde. Die Gewinnung von CRV und CAV erfolgte wie in 1.2 beschrieben.

CAV-Plaqueassays wurden gemäß 1.6 durchgeführt. Die nach 3 Tagen sichtbaren Plaques wurden isoliert und in 200 µl PBS mit 5% NCS überführt. Nach 3 Zyklen Ein- und Auftauen wurde die Suspension verwendet um Zellen zu infizieren, die dann auf die Anwesenheit des rekombinanten Herpessimplex Virus durch ß-Gal-Anfärbung und Expression der Adeno-assoziierten Virusproteine Rep oder Cap analysiert wurden. Ein positiver Plaque wurde ausgewählt und durch weitere nachfolgende Plaqueassay-Runden gereinigt. Auch wenn ein homogenes und reines rekombinantes Isolat bereits nach Runde 4 erhalten wurde, wurden weitere Plaquereinigungsrunden durchgeführt, um selbst kleinste Verunreingungen durch restlichen Wildtyp Herpes simplex Virus zu vermeiden. Alle positiven Plaques zeigten identische Muster an Rep oder Cap-Expression in der Westernblotanalyse.

Die Anwesenheit an Wildtyp HSV wurde durch Infektion verschieden großer Zellkulturschalen mit dem rekombinanten Virus und anschließendes das X-Gal Anfärben etwa 12 h p.i. untersucht. Dabei konnte keine Bildung von Wildtyp HSV angezeigt durch ungefärbte Bereiche infizierte Zellen beobachtet werden.

Das rekombinante HSV, hierin auch als rHSV/AAV bezeichnet, konnte in BHK-21 Rollerflaschen bis auf CRV-Titer von 1 bis 2 x 10^7 PFU/ml gezüchtet werden, verglichen zu etwa 1 x 10^8 PFU/ml, wenn Wildtyp HSV-1 1802 verwendet wurde. Die Reinheit aller rHSV/AAV-Präparationen wurde durch X-Gal-Anfärbung (siehe 1.7) analysiert. Auch bei Vermehrung von rHSV/AAV über mehrere Runden mit sehr geringen Infektionsmultiplizitäten wurde keine Reversion von rekombinantem HSV zu Wildtyp-HSV beobachtet. Unter diesen experimentellen Bedingungen würde evtl. vorhandenes Wildtyp-HSV das rHSV/AAV überwachsen, das - wie aus den obigen Titerangaben ersichtlich ist - geringfügige Wachstumsnachteile hat. Das isolierte rHSV/AAV ist dabei stabil und vermehrungsfähig. Aliquots der rHSV/AAV Präparationen wurden bei der European Collection of Cell Cultures CAMR, Salisbury, Wiltshire SP4 0IG, UK am 10. November 1997 hinterlegt und erhielten die vorläufige Zugangsnummer V97111302.

2.2 Expression von AAV Rep-Proteinen in mit rHSV/AAV infizierten BHK-Zellen

Bereits bei der Analyse während der Plaquereinigung zeigte sich, daß AAV-Proteine nach Infektion von Zellen mit rHSV/AAV exprimiert werden. Zur genaueren Analyse des Zeitverlaufs und der Expressionshöhe wurden BHK-21 Zellen mit rHSV/AAV in einer Infektionsmultiplizität (MOI) von 1 infiziert und bei den angegebenen Zeiten nach der Infektion geerntet. AAV Rep78 und Rep52 waren in BHK-21 Zellen bereits vier Stunden nach Infektion mit rHSV/AAV nachweisbar (Abb. 2A). Nach 8 h nach Infektion (8 h p.i.) waren alle vier Rep-Proteine sichtbar, wobei die Anteile vergleichbar einer Coinfektion von AAV Wildtyp und HSV-1 1802 waren. Die Expression der Rep-Proteine war sehr hoch und lag im Bereich einer produktiven Wildtyp-AAV Infektion in Gegenwart eines Helfervirus.

Dieses Ergebnis zeigt, daß die integrierte AAV Sequenz, die die authentischen AAV Promotoren enthält, durch die HSV-spezifischen

Proteine wie ein nichtintegriertes Wildtypgenom nach Coinfektion mit einem Helfervirus reguliert wird. Zusätzlich zeigen die Ergebnisse, daß ein produktiver HSV Lebenszyklus selbst durch einen sehr hohen Gehalt an Rep-Proteinen nicht signifikant inhibiert wird.

Da eine Infektion mit HSV sehr schnell den Wirtszellenmetabolismus übernimmt und schließlich die Zelle lysiert, wurde die Gegenwart von Rep-Proteinen in einem späten Stadium der Infektion untersucht. Das Ergebnis (Abb. 2B) zeigt an, daß die Expression von Rep-Proteinen zwischen 16 bis 24 h p.i. ein Plateau erreicht und Rep selbst in einem sehr späten Stadium (72 h) nach Infektion noch nachweisbar sind.

2.3 Expression von Cap-Proteinen

Zur effizienten Verpackung ist eine hohe Expression der Adeno-assoziierten Cap-Proteine erforderlich. Deshalb wurde der Zeitverlauf der AAV Cap-Expression in BHK-21 Zellen nach Infektion mit rHSV/AAV analysiert (Abb. 3). Das AAV VP3 Protein war bereits 0 h nach Infektion detektierbar (Abb. 3A), so daß es in das rHSV/AAV-Virion eingebaut werden kann. Zwischen 6 bis 8 h p.i. wurde eine Akkumulierung AAV VP Proteine gefunden, wobei die Mengen an VP1, VP2 und VP3 von einer Wildtyp AAV Infektion in Gegenwart von HSV-1 12 h nach Infektion nicht unterscheidbar waren (Abb. 3A). Dabei wurde eine entsprechende Expression der AAV VP Proteine erst initiiert, wenn ausreichende Gehalte an Rep-Proteinen, insbesondere Rep78 und Rep52 in den infizierten Zellen vorliegen (Abb. 2A). Die Expression der VP Proteine war von der Infektion bis zu 72 h nach Infektion hoch (Abb. 3B).

Zusammenfassend kann festgehalten werden, daß nach Infektion von BHK-21 Zellen mit rHSV/AAV hohe Mengen der VP-Proteine vorliegen, die in den Anteilen vergleichbar mit einer Coinfektion von Wildtyp AAV und HSV-1 sind.

Es wurde auch eine Expression der AAV-Proteine Cap und Rep in mit rHSV/AAV infizierten HeLa- oder Verozellen gefunden.

2.4 Nachweis von AAV Capsidstrukturen

Es wurde durch Immunofluoreszenzanalyse untersucht, ob die Expression der AAV Cap-Proteine VP1, VP2 und VP3 zur Verpackung ausreicht. Unter Verwendung eines Rep-spezifischen Antikörpers (1.8) wurde eine intensive nukleäre und zytoplasmatische Anfärbung von rHSV/AAV infizierten BHK-21 Zellen beobachtet (Abb. 4). Unter Verwendung eines Cap-spezifischen Antikörpers (1.8) wurde ein ähnliches Anfärbungsmuster mit etwas geringeren Intensitäten gefunden (Abb. 4). Auch mit dem AAV-Capsid-spezifischen Antikörper A20 (1.8) konnten positive Signale in rHSV/AAV-infizierten Zellen nachgewiesen werden (Abb. 4).

2.5 Verpackung von rekombinanten Adeno-assoziierten Virusvektoren mittels rHSV/AAV

Rekombinantes HSV/AAV unterstützt die Replikation und Verpackung von rekombinanten Adeno-assoziierten Virusvektoren, was unter Verwendung von lacZ- oder GFP-transduzierenden Adeno-assoziierten Vektoren gezeigt wurde.

Zur Bestimmung der tatsächlichen Zahl von Partikeln wurden BHK-21- oder Vero-Zellen mit rAAV-GFP (UF5) oder rAAV-GFP und ΔTR transfiziert und anschließend entweder mit rHSV/AAV oder HSV-1 1802 wie oben beschrieben, infiziert. Die Partikelzahl im Rohlysat wurde durch Dotblot bestimmt. Unter Verwendung des erfindungsgemäßen rHSV/AAV wurden 1×10^4 rAAV-GFP-Partikel/Zelle gebildet verglichen mit 8×10^3 Partikel/Zelle unter Verwendung des herkömmlichen Verfahrens.

Dazu wurden 14 cm Kulturschalen mit 100 µg UF5 oder 50 µg von jeweils UF5 und ΔTR transfiziert. Die transfizierten Zellen wurden entweder mit den rekombinanten HSV/AAV oder der HSV-1 Variante 1802 in einer MOI von 1 infiziert. Lysate wurden drei Tage p.i. hergestellt und auf die Zahl an physikalischen rAAV-GVP-Partikel analysiert. Die Membran wurde auf das [α-^{32}P] dCTP-markierte 731 bp NotI-Fragment von rAAV-GFP in einem Hybridisierungspuffer (Church et al. Proc. Natl. Acad. Sci. (USA) 81, (1984) 1991-1995) hybridisiert und bei 65°C inkubiert. Nach Waschen wurde der Filter freigelegt und die Flecken wurden ausgeschnitten. Die Flecken wurden in einem Packard Szintillationszähler gezählt und die Anzahl an Partikeln wurde unter Verwendung der Standards berechnet.

Die Ergebnisse sind in der folgenden Tabelle dargestellt.

Tabelle 1

Probe	Anzahl an Zellen	Anzahl rAAV Partikel	rAAV Partikel/Zelle
BHK x UF5 inf. rHSV/AAV	4×10^7	4×10^{11}	1×10^4
BHK x UF5/ΔTR inf. HSV-1	4×10^7	$3{,}2 \times 10^{11}$	8×10^3
Vero x UF5 inf. rHSV/AAV	3×10^7	$9{,}5 \times 10^{10}$	$3{,}2 \times 10^3$
Vero x UF5/ΔTR inf. HSV-1	3×10^7	4×10^{11}	$1{,}3 \times 10^4$

2.5 Reinheit und Stabilität der rHSV/AAV-Präparation

Die Bildung von Wildtyp AAV (wt AAV) während einer AAV-Vektorproduktion ist nicht unüblich (siehe z.B. Muzyczka, Curr. Topics. Microbiol. Immunol. 158 (1992) 97-129) und muß deshalb beim Verpacken sorgfältig überprüft werden. Insbesondere wenn die Herstellung eines Vektors in großem Maßstab angestrebt wird, muß die Bildung von Wildtyp AAV begrenzt und kontrolliert werden. Die in rHSV/AAV integrierten AAV

Sequenzen waren derart aufgebaut, daß sie frei von Sequenzelementen der invertierten terminalen Repetitionen (ITR) waren. Als Folge davon gibt es keine Sequenzüberlappungen zwischen rHSV/AAV und dem verwendeten AAV-GFP (UF5) was die Wahrscheinlichkeit eines Rekombinationsereignisses minimiert, das zur Bildung von wtAAV führen könnte. Um auszuschließen, daß wtAAV durch andere Prozesse, z.B. nichthomologe Rekombination gebildet wird, wurde ein rohes Verpackungslysat für infektiöses rAAV-GFP und wtAAV in einem Replikationscenterassay analysiert. Im Gegensatz zum Dotblot, der physikalische Partikel mißt, zeigt der Replikationscenterassay nur die infektiösen und vermehrungsfähigen Partikel.

Zwei verschiedene Konzentrationen von UF5 (10 µg oder 20 µg) oder 10 µg von jeweils UF5 und ΔTR wurden in 4 x 10^5 HeLa-Zellen unter Verwendung der Ca-Phosphat-Methode transfiziert. Etwa 20 h nach Transfektion wurden die Zellen mit rHSV in einer MOI von 1 (für UF5 allein) oder Adenovirus mit einer MOI von 3 (für UF5/ΔTR) infiziert. Die Zellen wurden 40 h p.i. geerntet und 3 Einfrier/Auftau-Zyklen unterworfen. Nach 30 min Inkubation bei 56 °C (zur Inaktivierung des Helfervirus) wurden die Zelltrümmer durch Zentrifugation pelletiert und der klare Überstand wurde gesammelt. Um den Replikationscenterassay durchzuführen wurden in 12-Well-Platten gezüchtete HeLa-Zellen nur mit Adenovirus (MOI = 20) oder mit Adenovirus (MOI = 20) und wtAAV (MOI = 4) infiziert. Anschließend wurden die Zellen mit 100 µl von jedem der zuvor hergestellten Rohlysate infiziert. Die Zellen wurden 24 h später geerntet, resuspendiert und mittels einer Vakuumvorrichtung auf Nitrozellulosemembranen überführt. Die Filter wurden mit einer gfp-spezifischen Sonde hybridisiert, um rAAV-infizierte Zellen nachzuweisen, und parallel mit einer rep-spezifischen Sonde, um Zellen sichtbar zu machen, die durch neu gebildetes wtAAV infiziert waren.

Die Ergebnisse zeigen, daß die Verwendung rHSV/AAV zusammen mit UF5 ausreichend ist, um rekombinante AAV-Vektoren zu bilden, die für eine

Infektion ähnlich der herkömmlichen Cotransfektion von UF5 und ΔTR infiziert mit Adenovirus kompetent sind (Abb. 5). Die Verwendung von entweder Adenovirus- oder Adenovirus- und wtAAV-infizierten HeLa-Zellen zeigt die Bildung von Wildtyp AAV an. In diesem Experiment war die Bildung wtAAV unter Verwendung des herkömmlichen Verfahrens sehr hoch. Im Gegensatz dazu wurden durch den neuen rHSV/AAV-Ansatz praktisch keine wtAAF-Partikel gebildet, wie durch Hybridisierung an die rep-spezifische Sonde angezeigt. Dies wurde auch durch Southern Blot-Analyse bestätigt, wobei in verschiedene Verpackungspräparationen keine replikativen Formen von wtAAV gefunden wurden.

2.7 Herstellung infektiöser rAAV-GFP-Partikel durch Infektion mit rHSV/AAV

Es wurde der Titer an infektiösen rAAV-GFP Partikeln bestimmt. Üblicherweise ist dieser etwa 1 x 10^3 niedriger als die Anzahl an physikalischen Partikeln. Rohlysate aus Ca-Phosphat-transfizierten BHK-21-Zellen wurden hierzu unter Verwendung des infektiösen Titerassays in 96-Well-Platten analysiert.

Zur Bestimmung der infektiösen Titer von wtAAV oder rAAV wurden HeLa-Zellen in 96-Well-Platten mit einem Volumen von 90 µl/Well gegeben. 10 µl der AAV enthaltenden Präparation wurden den Vertiefungen der ersten Reihe zugegen, vermischt und seriell 10fach für jeden der folgenden sieben Schritte verdünnt. Nach Inkubation für 12 bis 24 h wurden die transfizierten Zellen mit Adenovirus (MOI = 10-20) alleine infiziert, um auf wtAAV zu analysieren oder mit Adenovirus (MOI = 10-20) und wtAAV (MOI = 4), wenn der rAAv-Titer bestimmt wird. Wenn die Zellen ein vollständiges CPE zeigten, wurden sie dreimal eingefroren und aufgetaut. Die infektiösen Zellysate wurden auf eine Gene Screen® Membran übertragen. Nach Denaturieren der Membran für 5 min auf einer feuchten Schicht von Whatman-Papier, getränkt in 0,5 M NaOH, 1,5 M NaCl und Neutralisieren

durch Inkubation in 20 X SSC/0,5 M Tris, pH 7,5 für 5 min wurde die DNA auf der Membran UV-vernetzt. Die Membranen wurden zur Hybridisierung mit der entsprechenden Sonde gemäß Church et al., supra, verwendet und es wurde der rAAV oder wtAAV Titer berechnet.

Die Ergebnisse sind in Abb. 6 dargestellt und in Tabelle 2 zusammengefaßt.

Tabelle 2

Methode	10 µg UF5, rHSV/AAV MOI = 1	10 µg UF5, rHSV/AAV MOI = 0,1	10µg UF5, rHSV/AAV MOI = 0,01
inf. rAAV/ml	1×10^5	1×10^4	1×10^4

Methode	20 µg UF5, rHSV/AAV MOI = 1	20 µg UF5, rHSV/AAV MOI = 0,1	20 µg UF5, rHSV/AAV MOI = 0,01	10 µg UF5/10 µg ΔTR, HSV-1 1802 MOI = 1
inf.rAAV/ml	1×10^5	1×10^5	1×10^4	1×10^6

Ansprüche

1. Rekombinantes Herpesvirus,
dadurch gekennzeichnet,
daß es ein rep- und ein cap-Gen von Adeno-assoziierten Viren (AAV) in operativer Verküpfung mit einer Expressionskontrollsequenz enthält.

2. Rekombinantes Herpesvirus nach Anspruch 1,
dadurch gekennzeichnet,
daß es keine Reversion zum Wildtyp zeigt.

3. Rekombinantes Herpesvirus nach Anspruch 1 oder 2,
dadurch gekennzeichnet,
daß es weiterhin ein Reportergen umfaßt.

4. Rekombinantes Herpesvirus nach einem der vorhergehenden Ansprüche,
dadurch gekennzeichnet,
daß es ausgewählt ist aus der Gruppe der Herpesviridae umfassend Herpes-Simplex-Virus (HSV), Cytomegalovirus (CMV), Pseudorabiesvirus (PRV) und Epstein-Barr-Virus (EBV) und andere Mitglieder der Herpesvirusfamilie.

5. Rekombinantes Herpesvirus nach Anspruch 4,
dadurch gekennzeichnet,
daß es ein Herpes-Simplex-Virus (HSV) ist.

6. Rekombinantes Herpesvirus nach Anspruch 5,
dadurch gekennzeichnet,
daß es sich um die HSV-1 Mutante 1802 handelt.

7. Rekombinantes Herpesvirus nach einem der vorhergehenden Ansprüche,
dadurch gekennzeichnet,
daß es sich um eine vollständig oder teilweise replikationsdefiziente Mutante handelt.

8. Rekombinantes Herpesvirus nach einem der vorhergehenden Ansprüche,
dadurch gekennzeichnet,
daß die Insertion nicht die vollständige ITR-Sequenz von AAV umfaßt.

9. Rekombinantes Herpesvirus nach einem der vorhergehenden Ansprüche,
dadurch gekennzeichnet,
daß das rep- und das cap- Gen von AAV in der U_L oder der U_S-Region des Herpesvirus inseriert sind.

10. Verfahren zur Herstellung eines rekombinanten Herpesvirus nach einem der Ansprüche 1 bis 9,
dadurch gekennzeichnet,
daß man das rep- und das cap-Gen von AAV in das Genom eines Herpesvirus stabil integriert.

11. Verfahren nach Anspruch 10,
dadurch gekennzeichnet,
daß das rep- und das cap- Gen durch Restriktionsspaltung/Ligation oder durch homologe Rekombination in das Herpesvirus-Genom integriert werden.

12. Verfahren nach Anspruch 10 oder 11,
dadurch gekennzeichnet,
daß eine HSV-Mutante verwendet wird, die eine singuläre Restriktionsstelle aufweist.

13. Verfahren nach Anspruch 11,
dadurch gekennzeichnet,
daß eine vollständig oder teilweise replikationsdefiziente HSV-Mutante verwendet wird.

14. Nukleinsäure umfassend die zur Replikation von AAV-Viren erforderlichen Helferfunktionen eines Herpesvirusgenoms und darin insertiert ein rep- und ein cap-Gen von Adeno-assoziierten Viren (AAV) jeweils in operativer Verknüpfung einer Expressionskontrollsequenz.

15. Vektor,
dadurch gekennzeichnet,
daß er eine Nukleinsäure nach Anspruch 14 umfaßt.

16. Virale Zusammensetzung umfassend ein rekombinantes Herpesvirus nach einem der Ansprüche 1 bis 9.

17. Zusammensetzung nach Anspruch 16,
dadurch gekennzeichnet,
daß sie frei von Wildtyp-Herpesvirus ist.

18. Verfahren zur Herstellung von infektiösen AAV-Vektorpräparationen umfassend die Schritte:
(a) Bereitstellen eines viralen Vektors auf Basis von Adeno-assoziierten Viren (AAV),

(b) Bereitstellen eines rekombinanten Herpesvirus nach einem der Ansprüche 1 bis 9,

(c) Einbringen des AAV-Vektors von (a) und des rekombinanten Herpesvirus von (b) in eine Zelle,

(d) Vermehren des AAV-Vektors und

(e) Gewinnen einer infektiösen AAV-Vektorpräparation.

19. Verfahren nach Anspruch 18,
dadurch gekennzeichnet,
daß der AAV-Vektor und der rekombinante Herpesvirus durch Infektion in die Zelle eingebracht werden.

20. Verfahren nach Anspruch 18 oder 19,
dadurch gekennzeichnet,
daß man eine eingekapselte rAAV-Präparation gewinnt.

21. Verfahren nach einem der Ansprüche 18 bis 20,
dadurch gekennzeichnet,
daß ein replizierbares rekombinantes Herpesvirus verwendet wird.

22. Verfahren nach Anspruch 18 bis 20,
dadurch gekennzeichnet,
daß ein nichtreplizierbares rekombinantes Herpesvirus verwendet wird.

23. Zelle,
dadurch gekennzeichnet,
daß sie ein rekombinantes Herpesvirus nach einem der Ansprüche 1 bis 9 oder einen Vektor nach Anspruch 15 enthält.

24. Zelle nach Anspruch 23,
dadurch gekennzeichnet,
daß das rekombinante Herpesvirus oder der Vektor durch Infektion eingeführt worden ist.

25. Zelle nach Anspruch 23 oder 24,
dadurch gekennzeichnet,
daß sie weiterhin einen rekombinanten AAV-Vektor enthält.

26. Zelle nach Anspruch 25,
dadurch gekennzeichnet,
daß der AAV-Vektor eine heterologe DNA-Insertion enthält, die für ein therapeutisch wirksames Polypeptid kodiert.

27. Zelle nach einem der Ansprüche 23 bis 26,
dadurch gekennzeichnet,
daß es sich um eine BHK-, Vero- oder HeLa-Zelle handelt.

28. Verfahren zur Herstellung von infektiösen AAV-Vektorpräparationen, wobei ein AAV-Vektor und ein Helfervirus in eine Zelle eingebracht werden, der AAV-Vektor vermehrt und eine infektiöse AAV-Vektorpräparation aus der Zelle oder/und dem Kulturüberstand gewonnen wird,
dadurch gekennzeichnet,
daß der AAV-Vektor und das Helfervirus durch Infektion in die Zelle eingebracht werden.

Zusammenfassung

Es wird ein rekombinanter Herpesvirus beschrieben, der die rep- und cap-Gene von AAV umfaßt sowie ein Verfahren zur Herstellung von hochtitrigen, hochinfektiösen Adeno-assoziierten Virus-Vektor-Präparationen.

vo 01.07.1998

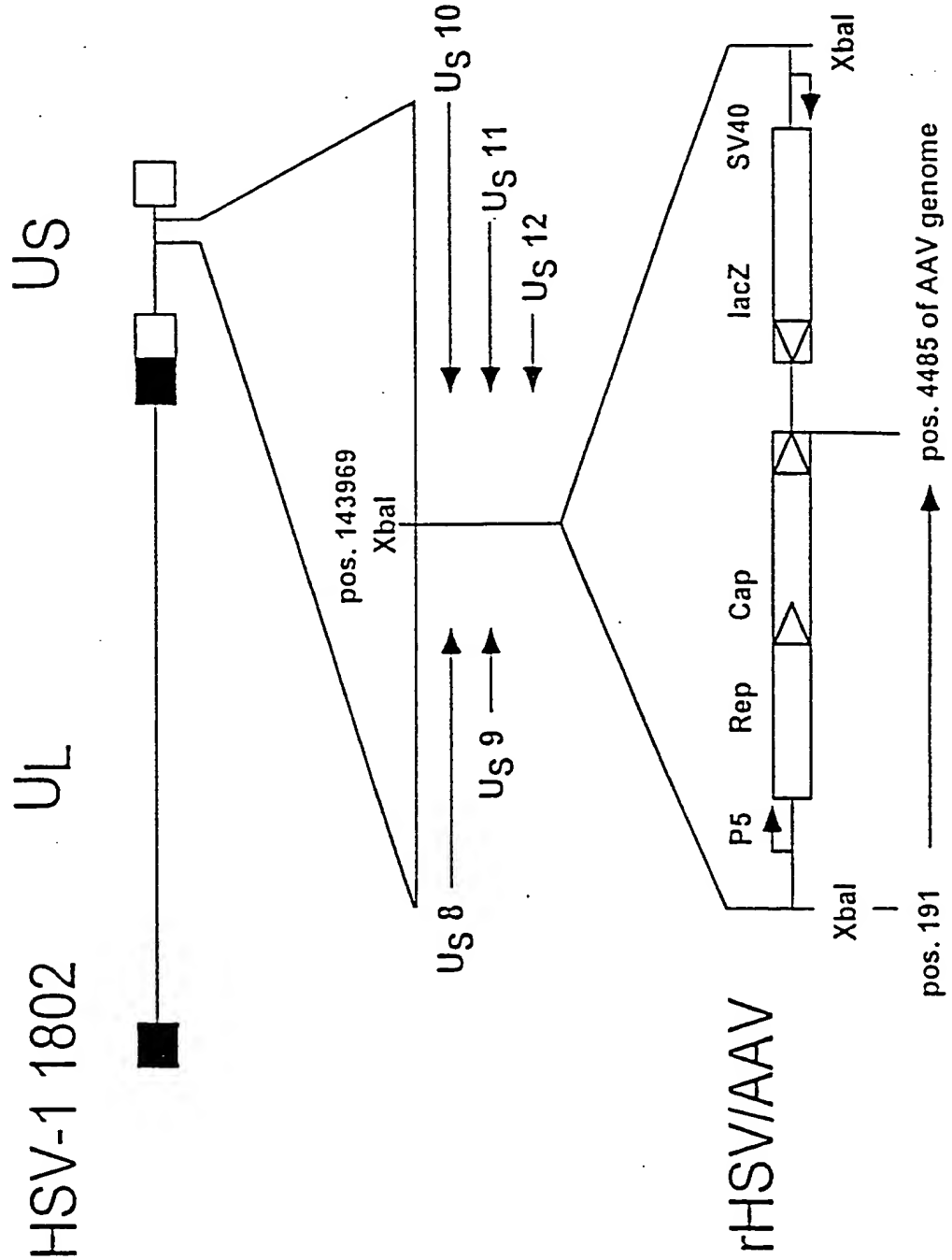
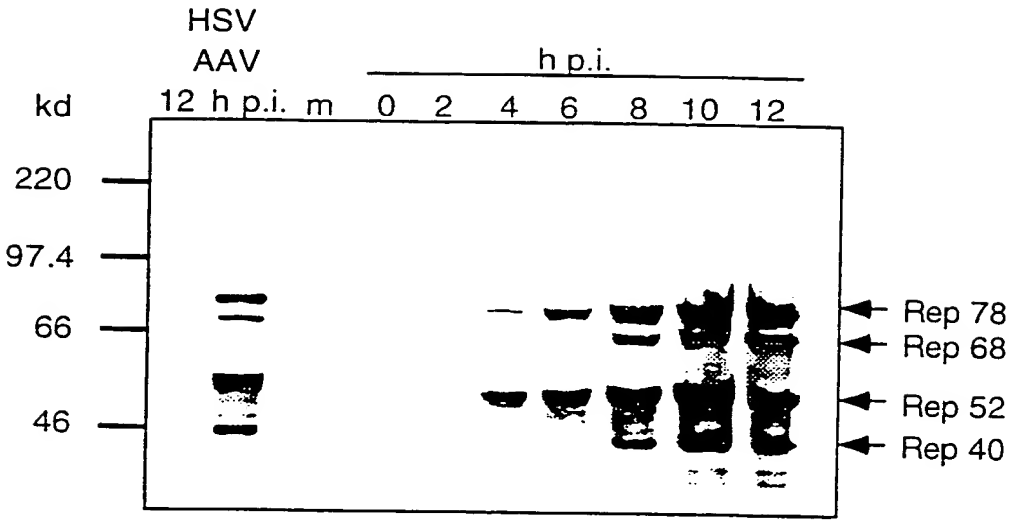

HSV-1 1802
US
UL
US 10
US 11
US 12
US 8
US 9
pos. 143969
XbaI
XbaI
pos. 191
P5
Rep
Cap
lacZ
SV40
XbaI
pos. 4485 of AAV genome
rHSV/AAV

Abbildung 1

A.



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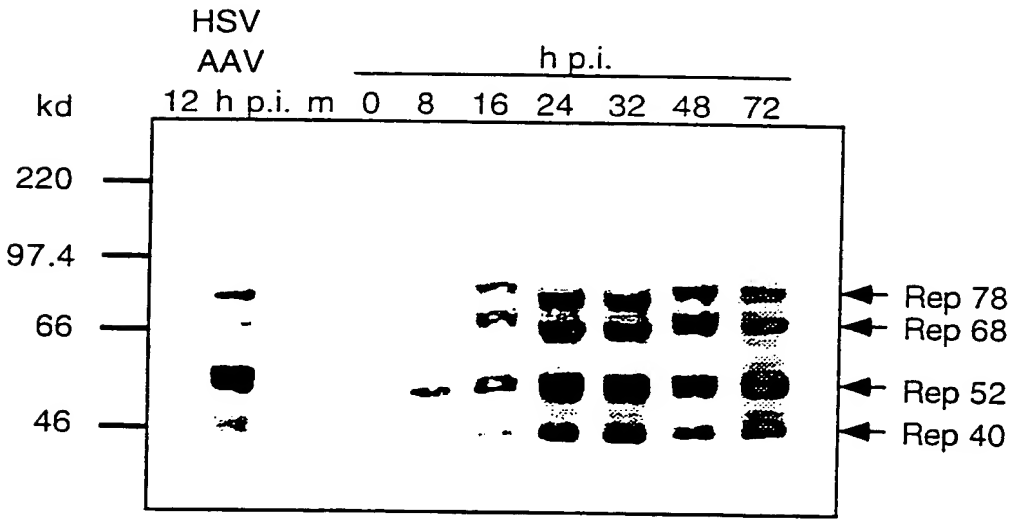
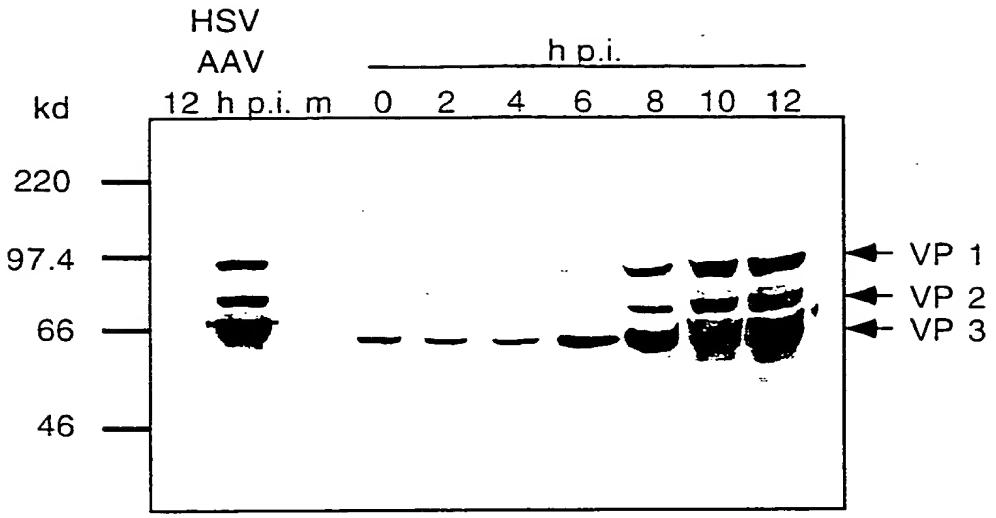


Abbildung 2



B.

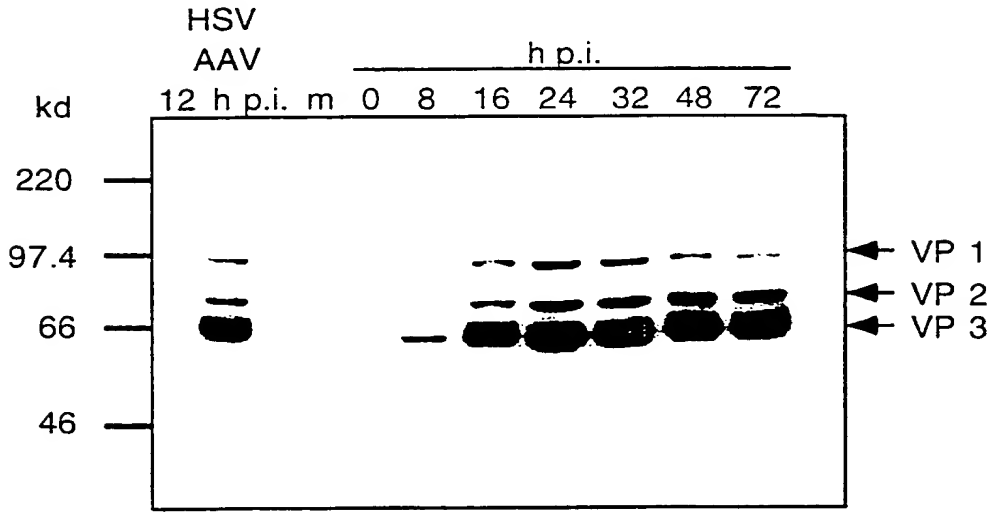
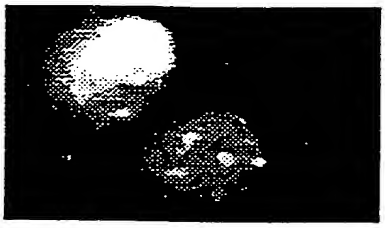
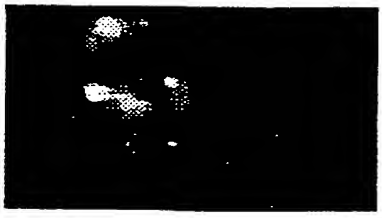


Abbildung 3

Rep-Antikörper (76.3)



Cap-Antikörper (B1)



Capsid-Antikörper (A20)

Abbildung 4

Abbildung 5

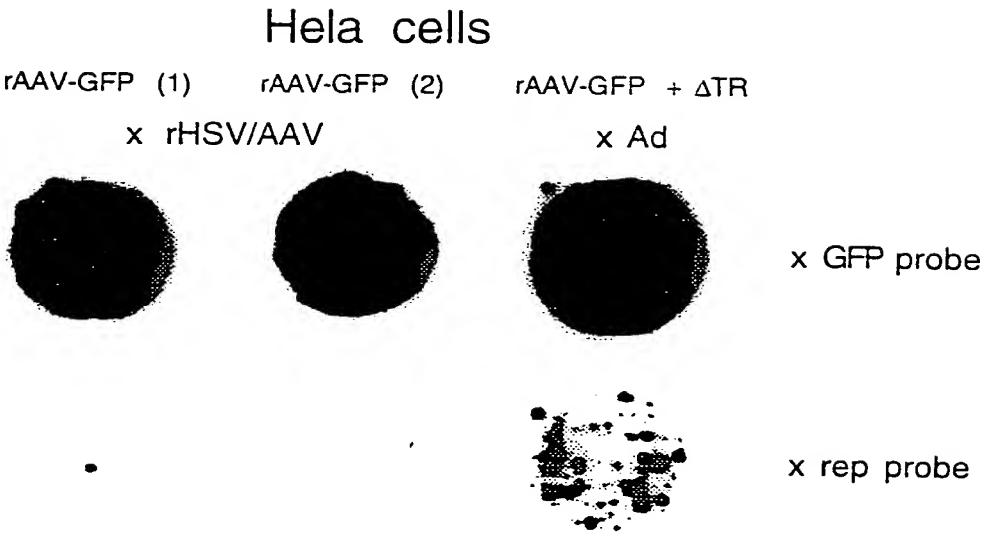
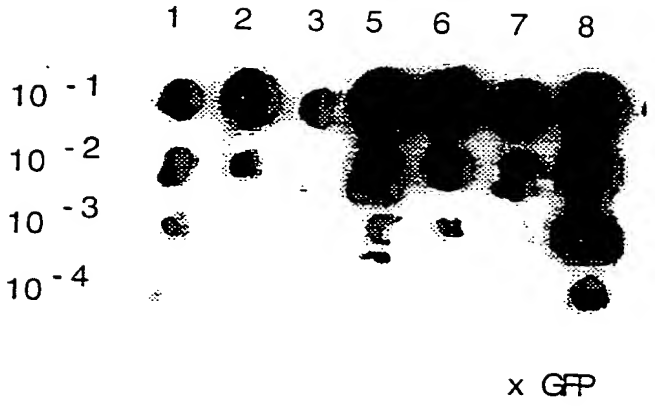

Hela cells
rAAV-GFP (1)
rAAV-GFP (2)
rAAV-GFP + ΔTR
x rHSV/AAV
x Ad
x GFP probe
x rep probe

Abbildung 6



VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES PATENTWESENS

PCT

INTERNATIONALER RECHERCHENBERICHT

(Artikel 18 sowie Regeln 43 und 44 PCT)

Aktenzeichen des Anmelders oder Anwalts	WEITERES VORGEHEN	siehe Mitteilung über die Übermittlung des internationalen Recherchenberichts (Formblatt PCT/ISA/220) sowie, soweit zutreffend, nachstehender Punkt 5
18397P WO		
Internationales Aktenzeichen	Internationales Anmeldedatum *(Tag/Monat/Jahr)*	(Frühestes) Prioritätsdatum *(Tag/Monat/Jahr)*
PCT/EP 98/ 05542	01/09/1998	06/07/1998
Anmelder		
HEILBRONN, Regine et al.		

Dieser internationale Recherchenbericht wurde von der Internationalen Recherchenbehörde erstellt und wird dem Anmelder gemäß Artikel 18 übermittelt. Eine Kopie wird dem Internationalen Büro übermittelt.

Dieser internationale Recherchenbericht umfaßt insgesamt 3 Blätter.

[X] Darüber hinaus liegt ihm jeweils eine Kopie der in diesem Bericht genannten Unterlagen zum Stand der Technik bei.

1. **Grundlage des Berichts**

   a. Hinsichtlich der **Sprache** ist die internationale Recherche auf der Grundlage der internationalen Anmeldung in der Sprache durchgeführt worden, in der sie eingereicht wurde, sofern unter diesem Punkt nichts anderes angegeben ist.

   [ ] Die internationale Recherche ist auf der Grundlage einer bei der Behörde eingereichten Übersetzung der internationalen Anmeldung (Regel 23.1 b)) durchgeführt worden.

   b. Hinsichtlich der in der internationalen Anmeldung offenbarten **Nucleotid- und/oder Aminosäuresequenz** ist die internationale Recherche auf der Grundlage des Sequenzprotokolls durchgeführt worden, das

   [ ] in der internationalen Anmeldung in Schriftlicher Form enthalten ist.

   [ ] zusammen mit der internationalen Anmeldung in computerlesbarer Form eingereicht worden ist.

   [ ] bei der Behörde nachträglich in schriftlicher Form eingereicht worden ist.

   [ ] bei der Behörde nachträglich in computerlesbarer Form eingereicht worden ist.

   [ ] Die Erklärung, daß das nachträglich eingereichte schriftliche Sequenzprotokoll nicht über den Offenbarungsgehalt der internationalen Anmeldung im Anmeldezeitpunkt hinausgeht, wurde vorgelegt.

   [ ] Die Erklärung, daß die in computerlesbarer Form erfaßten Informationen dem schriftlichen Sequenzprotokoll entsprechen, wurde vorgelegt.

2. [ ] **Bestimmte Ansprüche haben sich als nicht recherchierbar erwiesen** (siehe Feld I).

3. [ ] **Mangelnde Einheitlichkeit der Erfindung** (siehe Feld II).

4. Hinsichtlich der **Bezeichnung der Erfindung**

   [X] wird der vom Anmelder eingereichte Wortlaut genehmigt.

   [ ] wurde der Wortlaut von der Behörde wie folgt festgesetzt:

5. Hinsichtlich der **Zusammenfassung**

   [X] wird der vom Anmelder eingereichte Wortlaut genehmigt.

   [ ] wurde der Wortlaut nach Regel 38.2b) in der in Feld III angegebenen Fassung von der Behörde festgesetzt. Der Anmelder kann der Behörde innerhalb eines Monats nach dem Datum der Absendung dieses internationalen Recherchenberichts eine Stellungnahme vorlegen.

6. Folgende Abbildung der **Zeichnungen** ist mit der Zusammenfassung zu veröffentlichen: Abb. Nr. _____

   [ ] wie vom Anmelder vorgeschlagen

   [ ] weil der Anmelder selbst keine Abbildung vorgeschlagen hat.

   [ ] weil diese Abbildung die Erfindung besser kennzeichnet.

   [X] keine der Abb.

INTERNATIONALER RECHERCHENBERICHT

Internationales Aktenzeichen
PCT/EP 98/05542

A. KLASSIFIZIERUNG DES ANMELDUNGSGEGENSTANDES
IPK 6 C12N15/86 C12N7/01 C12N7/04 C12N5/10

Nach der Internationalen Patentklassifikation (IPK) oder nach der nationalen Klassifikation und der IPK

B. RECHERCHIERTE GEBIETE

Recherchierter Mindestprüfstoff (Klassifikationssystem und Klassifikationssymbole)
IPK 6 C12N

Recherchierte aber nicht zum Mindestprüfstoff gehörende Veröffentlichungen, soweit diese unter die recherchierten Gebiete fallen

Während der internationalen Recherche konsultierte elektronische Datenbank (Name der Datenbank und evtl. verwendete Suchbegriffe)

C. ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie°	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
X	WO 95 06743 A (UAB RESEARCH FOUNDATION) 9. März 1995 in der Anmeldung erwähnt siehe Zusammenfassung; Ansprüche 1,5,7,15,19,23,30,35; Beispiele VI,VII siehe Seite 6, Zeile 4 - Seite 7, Zeile 20 siehe Seite 10, Zeile 20 - Seite 11, Zeile 30 siehe Seite 12, Zeile 29 - Seite 13, Zeile 13 siehe Seite 15, Zeile 18 - Zeile 28 --- -/--	1,2,4,5, 7,9-21, 23-28

[X] Weitere Veröffentlichungen sind der Fortsetzung von Feld C zu entnehmen

[X] Siehe Anhang Patentfamilie

° Besondere Kategorien von angegebenen Veröffentlichungen :

"A" Veröffentlichung, die den allgemeinen Stand der Technik definiert, aber nicht als besonders bedeutsam anzusehen ist

"E" älteres Dokument, das jedoch erst am oder nach dem internationalen Anmeldedatum veröffentlicht worden ist

"L" Veröffentlichung, die geeignet ist, einen Prioritätsanspruch zweifelhaft erscheinen zu lassen, oder durch die das Veröffentlichungsdatum einer anderen im Recherchenbericht genannten Veröffentlichung belegt werden soll oder die aus einem anderen besonderen Grund angegeben ist (wie ausgeführt)

"O" Veröffentlichung, die sich auf eine mündliche Offenbarung, eine Benutzung, eine Ausstellung oder andere Maßnahmen bezieht

"P" Veröffentlichung, die vor dem internationalen Anmeldedatum, aber nach dem beanspruchten Prioritätsdatum veröffentlicht worden ist

"T" Spätere Veröffentlichung, die nach dem internationalen Anmeldedatum oder dem Prioritätsdatum veröffentlicht worden ist und mit der Anmeldung nicht kollidiert, sondern nur zum Verständnis des der Erfindung zugrundeliegenden Prinzips oder der ihr zugrundeliegenden Theorie angegeben ist

"X" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann allein aufgrund dieser Veröffentlichung nicht als neu oder auf erfinderischer Tätigkeit beruhend betrachtet werden

"Y" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann nicht als auf erfinderischer Tätigkeit beruhend betrachtet werden, wenn die Veröffentlichung mit einer oder mehreren anderen Veröffentlichungen dieser Kategorie in Verbindung gebracht wird und diese Verbindung für einen Fachmann naheliegend ist

"&" Veröffentlichung, die Mitglied derselben Patentfamilie ist

Datum des Abschlusses der internationalen Recherche	Absendedatum des internationalen Recherchenberichts
10. Mai 1999	28/05/1999

Name und Postanschrift der Internationalen Recherchenbehörde	Bevollmächtigter Bediensteter
Europäisches Patentamt, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Ceder, O

1

Formblatt PCT/ISA/210 (Blatt 2) (Juli 1992)

INTERNATIONALER RECHERCHENBERICHT

Internationales Aktenzeichen
PCT/EP 98/05542

C.(Fortsetzung) ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie°	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
X	WO 95 20671 A (RHONE POULENC RORER SA ;DESCAMPS VINCENT (FR); PERRICAUDET MICHEL) 3. August 1995 siehe Zusammenfassung; Ansprüche 1,4,15 siehe Seite 3, Zeile 25 - Zeile 30 siehe Seite 7, Zeile 17 - Zeile 24 ---	1,4,7,8, 10, 14-16, 18,22, 23,25,28
A	RIXON F J AND MCLAUCHLAN: "Insertion of DNA sequences at a unique restriction enzyme site engineered for vector purposes into the genome of herpes simplex virus type 1" JOURNAL OF GENERAL VIROLOGY, Bd. 113, Nr. 71, 1. Januar 1990, Seite 2931 2939 XP002079295 in der Anmeldung erwähnt siehe Zusammenfassung siehe Seite 2932, linke Spalte siehe Seite 2935, linke Spalte ---	3,6,12, 27
A	SRIVASTAVA A ET AL: "NUCLEOTIDE SEQUENCE AND ORGANIZATION OF THE ADENO-ASSOCIATED VIRUS 2 GENOME" JOURNAL OF VIROLOGY, Bd. 45, Nr. 2, 1. Februar 1983, Seiten 555-564, XP002058633 in der Anmeldung erwähnt ---	
A	CONWAY ET AL.: "Recombinant adeno-associated virus type 2 replication and packaging is entirely supported by herpes simplex virus type 1 amplicon expressing rep and cap" JOURNAL OF VIROLOGY, Bd. 71, Nr. 11, November 1997, Seiten 8780-8789, XP002102271 in der Anmeldung erwähnt siehe Zusammenfassung -----	1,4

1

INTERNATIONAL SEARCH REPORT

[redacted]tion on patent family members

[redacted]national Application No
PCT/EP 98/05542

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9506743 A	09-03-1995	AU 7565694 A	22-03-1995
WO 9520671 A	03-08-1995	FR 2716682 A	01-09-1995
		AU 1539595 A	15-08-1995
		CA 2181602 A	03-08-1995
		EP 0741793 A	13-11-1996
		FI 962990 A	26-07-1996
		JP 9509051 T	16-09-1997
		NO 962950 A	12-07-1996
		US 5789390 A	04-08-1998
		ZA 9500628 A	23-10-1995

VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES PATENTWESENS

Absender: MIT DER INTERNATIONALEN VORLÄUFIGEN PRÜFUNG BEAUFTRAGTE BEHÖRDE

KORRIGIERTE VERSION

An:

WEICKMANN WEICKMANN HUBER LISKA
PRECHTEL BÖHM WEISS TIESMEYER
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PCT

MITTEILUNG ÜBER DIE ÜBERSENDUNG DES INTERNATIONALEN VORLÄUFIGEN PRÜFUNGSBERICHTS
(Regel 71.1 PCT)

29. DEZ. 2000

Absendedatum *(Tag/Monat/Jahr)*	28.12.2000
Aktenzeichen des Anmelders oder Anwalts: 18397P WO	WICHTIGE MITTEILUNG

Internationales Aktenzeichen	Internationales Anmeldedatum *(Tag/Monat/Jahr)*	Prioritätsdatum *(Tag/Monat/Jahr)*
PCT/EP98/05542	01/09/1998	06/07/1998

Anmelder: HEILBRONN, Regine et al.

1. Dem Anmelder wird mitgeteilt, daß ihm die mit der internationalen vorläufigen Prüfung beauftragte Behörde hiermit den zu der internationalen Anmeldung erstellten internationalen vorläufigen Prüfungsbericht, gegebenenfalls mit den dazugehörigen Anlagen, übermittelt.

2. Eine Kopie des Berichts wird - gegebenenfalls mit den dazugehörigen Anlagen - dem Internationalen Büro zur Weiterleitung an alle ausgewählten Ämter übermittelt.

3. Auf Wunsch eines ausgewählten Amts wird das Internationale Büro eine Übersetzung des Berichts (jedoch nicht der Anlagen) ins Englische anfertigen und diesem Amt übermitteln.

4. **ERINNERUNG**

Zum Eintritt in die nationale Phase hat der Anmelder vor jedem ausgewählten Amt innerhalb von 30 Monaten ab dem Prioritätsdatum (oder in manchen Ämtern noch später) bestimmte Handlungen (Einreichung von Übersetzungen und Entrichtung nationaler Gebühren) vorzunehmen (Artikel 39 (1)) (siehe auch die durch das Internationale Büro im Formblatt PCT/IB/301 übermittelte Information).

Ist einem ausgewählten Amt eine Übersetzung der internationalen Anmeldung zu übermitteln, so muß diese Übersetzung auch Übersetzungen aller Anlagen zum internationalen vorläufigen Prüfungsbericht enthalten. Es ist Aufgabe des Anmelders, solche Übersetzungen anzufertigen und den betroffenen ausgewählten Ämtern direkt zuzuleiten.

Weitere Einzelheiten zu den maßgebenden Fristen und Erfordernissen der ausgewählten Ämter sind Band II des PCT-Leitfadens für Anmelder zu entnehmen.

Name und Postanschrift der mit der internationalen Prüfung beauftragten Behörde	Bevollmächtigter Bediensteter
Europäisches Patentamt D-80298 München Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Papiol Rovira, M Tel. +49 89 2399-7199

VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES PATENTWESENS

PCT

INTERNATIONALER VORLÄUFIGER PRÜFUNGSBERICHT

(Artikel 36 und Regel 70 PCT)

Aktenzeichen des Anmelders oder Anwalts	WEITERES VORGEHEN	siehe Mitteilung über die Übersendung des internationalen vorläufigen Prüfungsberichts (Formblatt PCT/IPEA/416)
18397P WO		
Internationales Aktenzeichen	Internationales Anmeldedatum *(Tag/Monat/Jahr)*	Prioritätsdatum *(Tag/Monat/Tag)*
PCT/EP98/05542	01/09/1998	06/07/1998
Internationale Patentklassifikation (IPK) oder nationale Klassifikation und IPK		
C12N15/86		
Anmelder		
HEILBRONN, Regine et al.		

1. Dieser internationale vorläufige Prüfungsbericht wurde von der mit der internationalen vorläufigen Prüfung beauftragten Behörde erstellt und wird dem Anmelder gemäß Artikel 36 übermittelt.

2. Dieser BERICHT umfaßt insgesamt 7 Blätter einschließlich dieses Deckblatts.

   ☒ Außerdem liegen dem Bericht ANLAGEN bei; dabei handelt es sich um Blätter mit Beschreibungen, Ansprüchen und/oder Zeichnungen, die geändert wurden und diesem Bericht zugrunde liegen, und/oder Blätter mit vor dieser Behörde vorgenommenen Berichtigungen (siehe Regel 70.16 und Abschnitt 607 der Verwaltungsrichtlinien zum PCT).

   Diese Anlagen umfassen insgesamt 1 Blätter.

3. Dieser Bericht enthält Angaben zu folgenden Punkten:

   - I ☒ Grundlage des Berichts
   - II ☐ Priorität
   - III ☐ Keine Erstellung eines Gutachtens über Neuheit, erfinderische Tätigkeit und gewerbliche Anwendbarkeit
   - IV ☐ Mangelnde Einheitlichkeit der Erfindung
   - V ☒ Begründete Feststellung nach Artikel 35(2) hinsichtlich der Neuheit, der erfinderischen Tätigkeit und der gewerblichen Anwendbarkeit; Unterlagen und Erklärungen zur Stützung dieser Feststellung
   - VI ☐ Bestimmte angeführte Unterlagen
   - VII ☐ Bestimmte Mängel der internationalen Anmeldung
   - VIII ☒ Bestimmte Bemerkungen zur internationalen Anmeldung

Datum der Einreichung des Antrags	Datum der Fertigstellung dieses Berichts
04/02/2000	28.12.2000
Name und Postanschrift der mit der internationalen vorläufigen Prüfung beauftragten Behörde:	Bevollmächtigter Bediensteter
Europäisches Patentamt D-80298 München Tel. +49 89 2399 - 0 Tx: 523656 epmu d Fax: +49 89 2399 - 4465	Celler, J Tel. Nr. +49 89 2399 7336

INTERNATIONALER VORLÄUFIGER PRÜFUNGSBERICHT

Internationales Aktenzeichen PCT/EP98/05542

I. Grundlage des Berichts

1. Dieser Bericht wurde erstellt auf der Grundlage (*Ersatzblätter, die dem Anmeldeamt auf eine Aufforderung nach Artikel 14 hin vorgelegt wurden, gelten im Rahmen dieses Berichts als "ursprünglich eingereicht" und sind ihm nicht beigefügt, weil sie keine Änderungen enthalten.*):
Beschreibung, Seiten:

1-29	ursprüngliche Fassung	

Patentansprüche, Nr.:

2-13,15-28	ursprüngliche Fassung	
1,14	mit Telefax vom	16/10/2000

Zeichnungen, Blätter:

1/5-5/5	ursprüngliche Fassung	

2. Hinsichtlich der **Sprache**: Alle vorstehend genannten Bestandteile standen der Behörde in der Sprache, in der die internationale Anmeldung eingereicht worden ist, zur Verfügung oder wurden in dieser eingereicht, sofern unter diesem Punkt nichts anderes angegeben ist.

   Die Bestandteile standen Behörde in der Sprache: , zur Verfügung bzw. wurden in dieser Sprache eingereicht; dabei handelt es sich um

   - ☐ die Sprache der Übersetzung, die für die Zwecke der internationalen Recherche eingereicht worden ist (nach Regel 23.1(b)).
   - ☐ die Veröffentlichungssprache der internationalen Anmeldung (nach Regel 48.3(b)).
   - ☐ die Sprache der Übersetzung, die für die Zwecke der internationalen vorläufigen Prüfung eingereicht worden ist (nach Regel 55.2 und/oder 55.3).

3. Hinsichtlich der in der internationalen Anmeldung offenbarten **Nucleotid- und/oder Aminosäuresequenz** ist die internationale vorläufige Prüfung auf der Grundlage des Sequenzprotokolls durchgeführt worden, das:

   - ☐ in der internationalen Anmeldung in schriftlicher Form enthalten ist.
   - ☐ zusammen mit der internationalen Anmeldung in computerlesbarer Form eingereicht worden ist.
   - ☐ bei der Behörde nachträglich in schriftlicher Form eingereicht worden ist.
   - ☐ bei der Behörde nachträglich in computerlesbarer Form eingereicht worden ist.
   - ☐ Die Erklärung, dass das nachträglich eingereichte schriftliche Sequenzprotokoll nicht über den Offenbarungsgehalt der internationalen Anmeldung im Anmeldezeitpunkt hinausgeht, wurde vorgelegt.
   - ☐ Die Erklärung, dass die in computerlesbarer Form erfassten Informationen dem schriftlichen Sequenzprotokoll entsprechen, wurde vorgelegt.

4. Aufgrund der Änderungen sind folgende Unterlagen fortgefallen:

   ☐ Beschreibung, Seiten:

   ☐ Ansprüche, Nr.:

   ☐ Zeichnungen, Blatt:

5. ☐ Dieser Bericht ist ohne Berücksichtigung (von einigen) der Änderungen erstellt worden, da diese aus den angegebenen Gründen nach Auffassung der Behörde über den Offenbarungsgehalt in der ursprünglich eingereichten Fassung hinausgehen (Regel 70.2(c)).

   (Auf Ersatzblätter, die solche Änderungen enthalten, ist unter Punkt 1 hinzuweisen;sie sind diesem Bericht beizufügen).

6. Etwaige zusätzliche Bemerkungen:

V. Begründete Feststellung nach Artikel 35(2) hinsichtlich der Neuheit, der erfinderischen Tätigkeit und der gewerblichen Anwendbarkeit; Unterlagen und Erklärungen zur Stützung dieser Feststellung

1. Feststellung

Neuheit (N)	Ja:	Ansprüche	1 - 27
	Nein:	Ansprüche	28
Erfinderische Tätigkeit (ET)	Ja:	Ansprüche	1 - 27
	Nein:	Ansprüche	28
Gewerbliche Anwendbarkeit (GA)	Ja:	Ansprüche	1 - 28
	Nein:	Ansprüche	

2. Unterlagen und Erklärungen
   siehe Beiblatt

VIII. Bestimmte Bemerkungen zur internationalen Anmeldung

Zur Klarheit der Patentansprüche, der Beschreibung und der Zeichnungen oder zu der Frage, ob die Ansprüche in vollem Umfang durch die Beschreibung gestützt werden, ist folgendes zu bemerken:
siehe Beiblatt

Zu Punkt V

Begründete Feststellung nach Artikel 35(2) hinsichtlich der Neuheit, der erfinderischen Tätigkeit und der gewerblichen Anwendbarkeit; Unterlagen und Erklärungen zur Stützung dieser Feststellung

Diese Anmeldung bezieht sich auf ein rekombinantes Herpesvirus und ein Verfahren zu dessen Herstellung. Das Herpesvirus dient weiter als ein Helfervirus bei der Herstellung rekombinanter Adeno-assoziierten Viren (AAV), die für Einsatz in Forschung und Therapie gedacht sind. Weitere Ansprüche sind auf entsprechende Zellen und Nukleinsäuren gerichtet.

Es wird auf die folgenden Dokumente verwiesen:

D1: CONWAY ET AL.: "Recombinant adeno-associated virus type 2 replicaltion and packaging is entirely supported by herpes simplex virus type 1 amplicon expressing rep and cap" JOURNAL OF VIROLOGY, Bd. 71, Nr. 11, November 1997

1. D1 beschreibt ein Verfahren zur Herstellung eines rekombinanten Herpes-Simplex-Virus Typ 1 Amplikons. Ein DNS-Konstrukt wurde hergestellt, das die zur Replikation von AAV erforderlichen Helferfunktionen eines Herpersvirusgenoms und darin inseriert ein rep- und cap-Gen von AAV jeweils in operativer Verknüpfung mit ihrer nativen Expressionskontrollsequenz umfaßt (z. B. Seite 8781, rechte Spalte, Zeile 25 - 56 und Seite 8780, Zeile 17 - 25). Die Konstruktion erfolgte durch *Xbal*-Restriktionspaltung eines rep- und cap-Gen kodierenden Fragmentes und folgende Ligation mit einem viralen Vektor, der eine singuläre *Xbal*-Restriktionstelle hat (Seite 8781, rechte Spalte, Zeile 25 - 56). Die singuläre *Xbal*-Restriktionstelle in dem viralen Vektor von D1 verbindet das HSV-genomische DNS-Fragment mit der DNS des pUC-basierenden Vektors. Daher wird davon ausgegangen, daß die in D1 beschriebene Insertion des rep- und cap-Gen kodierenden Fragmentes nicht im Genom des Herpesvirus integriert ist

sondern das rep- und cap-Gen kodierenden Fragmente neben dem HSV-genomischen Fragment inseriert ist. Da das Verfahren der vorliegenden Ansprüche 10 - 13, das rekombinante HSV der Ansprüche 1 - 9, die Nukleinsäure des Anspruchs 14 und der Vektor des Anspruchs 15 dadurch gekennzeichnet sind, daß das rep- und cap-Gen sich auf einer Insertion befinden, die im Genom des Herpesvirus (und nicht neben dem genomischen Fragment des Herpesvirus) inseriert ist, unterscheidet sich das in D1 offenbarte Verfahren und das DNS-Konstrukt von dem Verfahren und dem DNS-Konstrukt der vorliegenden Anmeldung und daher sind die Ansprüche 1 - 15 als neu anzusehen (Art. 33(2) PCT).

2. Darüberhinaus zeigt die Analyse in D1, daß die virale Zusammensetzung neben dem rekombinanten Virus - HSV-RC/*d27*, auch Wildtyp-Herpesvirus enthält (Seite 8782, linke Spalte, Zeilen 27 - 39). Dagegen ist das rekombinante HSV der vorliegenden Ansprüche 1 - 9 Wildtyp-Herpesvirus frei und homogen. Daher sind, zum Beispiel, die Mengen des rekombinanten HSV der vorliegenden Anmeldung einfacher zu bestimmen und besser kontrollierbar gegenüber denen von D1. Die Nukleinsäure des Anspruchs 14 und der Vektor des Anspruchs 15, die im Verfahren der Ansprüche 10 -13 verwendbar sind, dienen der Herstellung der rekombinanten HSV nach Ansprüchen 1 - 9 und sind damit durch den selben Vorteil gekennzeichnet, i.e. das hergestellte, rekombinante HSV ist Wildtyp-Herpesvirus frei. Somit sind die Ansprüche 1 - 15 als erfinderisch anzusehen (Art. 33(3) PCT).

3. Da die Ansprüche 16 - 27 entweder direkt oder indirekt von Ansprüchen 1- 9 abhängen, sind die Ansprüche 16 - 27 ebenfalls als neu und erfinderisch anzusehen (Art. 33(2) und (3) PCT).

4. Hinsichtlich des unabhängigen Anspruchs 28 wird der Anmelder darauf hingewiesen, daß das rekombinante Herpes-Simplex-Virus Typ 1 Amplikon von D1 mit Einsatz eines Helfervirus in infektöse Hüllen verpackt werden kann. Da auf diese Weise das Amplikon einen kompleten Lebenszyklus eines Virus, i. e. Vermehrung, Verpackung und Infektion, durchlaufen kann, kann das Amplikon als Virus gesehen werden. Der Begriff "Virus" hat sehr großen Umfang für einen Fachmann. Ein Virus kann DNS oder RNS enthalten, kann tierische, menschliche

als auch pflanzliche Zellen zur Vermehrung benötigen. Die Frage, ob Phagen, die bakterielle Zellen als Wirt nutzen zu den Viren zu zählen sind, kann nicht eindeutig beantwortet werden. Weiterhin, sind im Stand der Technik "Viren" beschrieben, die in ihrem eigenen Genom nicht alle Gene haben, die für das Durchlaufen des kompletten Lebenszyklus notwendig sind. Solche Viren sind abhängig von verschiedenen Helferfunktionen, die von den anderen Viren bereitgestellt werden müssen, sie sind aber trotzdem, für den Fachmann unter dem Begriff "Virus" bekannt. Zum Beispiel, Hepatitis Delta Virus (HDV), das auf die Hilfe vom Hepatitis B Virus (HBV) angewiesen ist oder Satellitvirus des "Maize White Line Mosaic Virus", dessen Lebenszyklus auf der Hilfe von "Maize White Line Mosaic Virus" beruht. Daher kann das Amplikon von D1 auch als Virus, beziehungsweise Helfervirus angesehen werden.

Das Amplikon wird in D1 zur Produktion von infektiösen AAV-Vektorpräparationen als Helfervirus eingesetzt. Das Verfahren umfaßt das Einbringen des rekombinanten AAV-Vektors und des rekombinanten Helfervirus durch Infektion in HeLa-Zellen (Seite 8786, rechte Spalte, Zeilen 21 - 37). Dadurch entstehen Zellen, die beide Vektoren enthalten und aus denen eine infektiöse AAV-Präparation gewonnen wird (Seite 8786, rechte Spalte, Zeilen 21 - 37 und Seite 8788, linke Spalte, Zeilen 42 - 44). Somit sind die technischen Merkmale des in D1 offenbarten Verfahrens zur Herstellung rekombinanter AA-Viren identisch mit den Merkmalen des Verfahrens, das den Gegenstand des Anspruchs 28 darstellt. Demzufolge ist der Anspruch 28 nicht neu und nicht erfinderisch (Art. 33(2) und (3) PCT).

Zu Punkt VIII
Bestimmte Bemerkungen zur internationalen Anmeldung

Ansprüche 2 und 10 entsprechen nicht den Erfordernissen des Art. 6 PCT, weil der Gegenstand des Schutzbegehrens nicht klar definiert ist. In den Ansprüchen wird versucht, den Gegenstand durch das zu erreichende Ergebnis zu definieren; damit wird aber lediglich die zu lösende Aufgabe angegeben. Deswegen ist es

unklar wie ein Fachmann die rep- und cap-Gene stabil inseriert und das Virus, das keine Reversion zeigt, herstellen soll. Der Anmelder wird darauf hingewiesen, daß einem Fachmann klar ist, wie man die Virusstabilität überprüft. Es ist jedoch unklar, welche technischen Merkmale berücksichtigt werden müssen um ein stabiles, rekombinantes Virus, das keine Reversion zeigt, herzustellen.

WWmy
18397P WO

PCT/EP98/05542
Prof. Dr. Regine Heilbronn

Neue Ansprüche

1. Rekombinantes Herpesvirus,
dadurch gekennzeichnet,
dass es ein rep- und ein cap-Gen von Adeno-assoziierten Viren (AAV) in operativer Verknüpfung mit einer Expressionskontrollsequenz enthält, wobei sich das rep- und das cap-Gen auf einer Insertion befinden, die im Genom des Herpesvirus integriert ist.

14. Nukleinsäure umfassend die zur Replikation von AAV-Viren erforderlichen Helferfunktionen eines Herpesvirusgenoms und darin insertiert ein rep- und ein cap-Gen von Adeno-assoziierten Viren (AAV) jeweils in operativer Verknüpfung einer Expressionskontrollsequenz, wobei sich das rep- und das cap-Gen auf einer Insertion befinden, die im Genom des Herpesvirus integriert ist.

PCT

ANTRAG

Der Unterzeichnete beantragt, daß die vorliegende internationale Anmeldung nach dem Vertrag über die internationale Zusammenarbeit auf dem Gebiet des Patentwesens behandelt wird.

Vom Anmeldeamt auszufüllen

Internationales Aktenzeichen: PCT/EP 98/05542

Internationales Anmeldedatum: (01.09.98) 01 SEP 1998

Name des Anmeldeamts und "PCT International Application": EUROPEAN PATENT OFFICE PCT INTERNATIONAL APPLICATION

Aktenzeichen des Anmelders oder Anwalts (falls gewünscht, max. 12 Zeichen): 18397P WO

Feld Nr. I BEZEICHNUNG DER ERFINDUNG

Rekombinante Herpesviren für die Erzeugung rekombinanter Adeno-assoziierter-Viren

Feld Nr. II ANMELDER

Name und Anschrift: *(Familienname, Vorname; bei juristischen Personen vollständige amtliche Bezeichnung. Bei der Anschrift sind die Postleitzahl und der Name des Staats anzugeben. Der in diesem Feld in der Anschrift angegebene Staat ist der Staat des Sitzes oder Wohnsitzes des Anmelders, sofern nachstehend kein Staat des Sitzes oder Wohnsitzes angegeben ist.)*

HEILBRONN, Regine
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DE

[XX] Diese Person ist gleichzeitig Erfinder

Telefonnr.:

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Fernschreibnr.:

Staatsangehörigkeit (Staat): DE

Sitz oder Wohnsitz (Staat): DE

Diese Person ist Anmelder für folgende Staaten: [X] alle Bestimmungsstaaten [ ] alle Bestimmungsstaaten mit Ausnahme der Vereinigten Staaten von Amerika [ ] nur die Vereinigten Staaten von Amerika [ ] die im Zusatzfeld angegebenen Staaten

Feld Nr. III WEITERE ANMELDER UND/ODER (WEITERE) ERFINDER

Name und Anschrift: *(Familienname, Vorname; bei juristischen Personen vollständige amtliche Bezeichnung. Bei der Anschrift sind die Postleitzahl und der Name des Staats anzugeben. Der in diesem Feld in der Anschrift angegebene Staat ist der Staat des Sitzes oder Wohnsitzes des Anmelders, sofern nachstehend kein Staat des Sitzes oder Wohnsitzes angegeben ist.)*

SCHETTER, Christian
Overbergstraße 19
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DE

Diese Person ist:

[ ] nur Anmelder

[X] Anmelder und Erfinder

[ ] nur Erfinder *(Wird dieses Kästchen angekreuzt, so sind die nachstehenden Angaben nicht nötig.)*

Staatsangehörigkeit (Staat): DE

Sitz oder Wohnsitz (Staat): DE

Diese Person ist Anmelder für folgende Staaten: [ ] alle Bestimmungsstaaten [ ] alle Bestimmungsstaaten mit Ausnahme der Vereinigten Staaten von Amerika [X] nur die Vereinigten Staaten von Amerika [ ] die im Zusatzfeld angegebenen Staaten

[ ] Weitere Anmelder und/oder (weitere) Erfinder sind auf einem Fortsetzungsblatt angegeben.

Feld Nr. IV ANWALT ODER GEMEINSAMER VERTRETER; ODER ZUSTELLANSCHRIFT

Die folgende Person wird hiermit bestellt/ist bestellt worden, um für den (die) Anmelder vor den zuständigen internationalen Behörden in folgender Eigenschaft zu handeln als: [X] Anwalt [ ] gemeinsamer Vertreter

Name und Anschrift: *(Familienname, Vorname; bei juristischen Personen vollständige amtliche Bezeichnung. Bei der Anschrift sind die Postleitzahl und der Name des Staats anzugeben.)*

Weickmann H., Weickmann F.A., Huber B.,
Liska H., Prechtel J., Böhm B., Weiß W.,
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Fernschreibnr.: 522 621 wepat d

[ ] Zustellanschrift: Dieses Kästchen ist anzukreuzen, wenn kein Anwalt oder gemeinsamer Vertreter bestellt ist und statt dessen im obigen Feld eine spezielle Zustellanschrift angegeben ist.

INTERNATIONALER RECHERCHENBERICHT

Angaben zu Veröffentlichungen, die zur selben Patentfamilie gehören

Internationales Aktenzeichen
PCT/EP 98/05542

Im Recherchenbericht angeführtes Patentdokument	Datum der Veröffentlichung	Mitglied(er) der Patentfamilie	Datum der Veröffentlichung
WO 9506743 A	09-03-1995	AU 7565694 A	22-03-1995
WO 9520671 A	03-08-1995	FR 2716682 A	01-09-1995
		AU 1539595 A	15-08-1995
		CA 2181602 A	03-08-1995
		EP 0741793 A	13-11-1996
		FI 962990 A	26-07-1996
		JP 9509051 T	16-09-1997
		NO 962950 A	12-07-1996
		US 5789390 A	04-08-1998
		ZA 9500628 A	23-10-1995

09/720252

Translation

PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 18397P WO	FOR FURTHER ACTION	See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)
International application No. PCT/EP98/05542	International filing date (*day/month/year*) 01 September 1998 (01.09.98)	Priority date (*day/month/year*) 06 July 1998 (06.07.98)
International Patent Classification (IPC) or national classification and IPC C12N 15/86, 7/01, 7/04, 5/10		
Applicant HEILBRONN, Regine		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.

2. This REPORT consists of a total of 7 sheets, including this cover sheet.

☒ This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of 1 sheets.

3. This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☐ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
- IV ☐ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☐ Certain documents cited
- VII ☐ Certain defects in the international application
- VIII ☒ Certain observations on the international application

Date of submission of the demand	Date of completion of this report
04 February 2000 (04.02.00)	28 December 2000 (28.12.2000)
Name and mailing address of the IPEA/EP Facsimile No.	Authorized officer Telephone No.

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No.
PCT/EP98/05542

I. Basis of the report

1. This report has been drawn on the basis of (*Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments.*):

☐ the international application as originally filed.

☒ the description, pages 1-29, as originally filed,
pages _____, filed with the demand,
pages _____, filed with the letter of _____.
pages _____, filed with the letter of _____.

☒ the claims, Nos. 2-13,15-28, as originally filed,
Nos. _____, as amended under Article 19,
Nos. _____, filed with the demand,
Nos. 1,14, filed with the letter of 16 October 2000 (16.10.2000),
Nos. _____, filed with the letter of _____.

☒ the drawings, sheets/fig 1/5-5/5, as originally filed,
sheets/fig _____, filed with the demand,
sheets/fig _____, filed with the letter of _____,
sheets/fig _____, filed with the letter of _____.

2. The amendments have resulted in the cancellation of:

☐ the description, pages _____
☐ the claims, Nos. _____
☐ the drawings, sheets/fig _____

3. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the Supplemental Box (Rule 70.2(c)).

4. Additional observations, if necessary:

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No.
PCT/EP 98/05542

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Claims	1-27	YES
	Claims	28	NO
Inventive step (IS)	Claims	1-27	YES
	Claims	28	NO
Industrial applicability (IA)	Claims	1-28	YES
	Claims		NO

2. Citations and explanations

This application concerns a recombinant herpes virus and a method for producing the same. The herpes virus also serves as helper virus when producing recombinant adeno-associated viruses (AAV) designed for use in research and therapy. Other claims are directed to corresponding cells and nucleic acids.

This report makes reference to the following document:

D1: CONWAY ET AL.: "Recombinant adeno-associated virus type 2 replication and packaging is entirely supported by *herpes simplex* virus type 1 amplicon expressing rep and cap", JOURNAL OF VIROLOGY, Vol. 71, No. 11, November 1997.

1. D1 describes a method for producing a recombinant *Herpes simplex* virus type 1 amplicon. A DNA construct was produced comprising the helper functions of a herpes virus genome required for AAV replication, and AAV rep and cap genes, each operationally linked to its native expression control sequence, are inserted therein (e.g. page 8781, right-hand column, lines 25-56, and page 8780, lines 17-25). Construction was carried out by *XbaI*

restriction cleavage of a fragment that codes for a rep and cap gene, then ligation with a viral vector with a singular *XbaI* restriction site (page 8781, right-hand column, lines 25-56). The singular *XbaI* restriction site in the viral vector of D1 connects the HSV genomic DNA fragment with the DNA of the pUC-based vector. Consequently, it is assumed that the insertion of the fragment coding for the rep and cap genes described in D1 is not integrated in the genome of the herpes virus, but rather that the fragments coding for the rep and cap genes are inserted beside the HSV genomic fragment. Since the method of the present Claims 10-13, the recombinant HSV as per Claims 1-9, the nucleic acid as per Claim 14 and the vector as per Claim 15 are characterised in that the rep and cap genes are located on an insertion inserted in the genome of the herpes virus (and not beside the genomic fragment of the herpes virus), the method and DNA construct of D1 differ from the method and DNA construct of the present application, and Claims 1-15 should therefore be considered novel (PCT Article 33(2)).

2. Furthermore, the analysis in D1 shows that the viral composition also contains wild type herpes virus, besides the recombinant virus HSV-RC/*d27* (page 8782, left-hand column, lines 27-39). This is not the case of the recombinant HSV as per the present Claims 1-9, which is free from wild type herpes virus and is homogeneous. Consequently, the quantities of recombinant HSV, for example, are easier to determine and to control in the present application than in D1. The nucleic acids as per Claim 14 and the vector as per Claim 15, which can be used in the method as per Claims 10-13, serve for producing the

recombinant HSV as per Claims 1-9 and are therefore characterised by the same advantage, that is, the thus produced recombinant HSV is free from wild type herpes virus. Claims 1-15 should therefore be considered inventive (PCT Article 33(3)).

3. Since Claims 16-27 are either directly or indirectly dependent on Claims 1-9, Claims 16-27 should also be considered novel and inventive (PCT Article 33(2) and (3)).

4. Regarding independent Claim 28, the applicant is advised that the recombinant *Herpes simplex* virus type 1 amplicon of D1 can be packaged in infectious envelopes using a helper virus. Since the amplicon chan thus run through the entire life cycle of a virus, that is reproduction, packaging and infection, the amplicon can be regarded as a virus. The term "virus" has a very large scope for a person skilled in the art. A virus can contain DNA or RNA, can require animal, human and also plant cells for reproduction. It is not possible to give an unambiguous answer to the question of whether phages which use bacterial cells as hosts should be counted among the viruses. Moreover, the prior art describes "viruses" which do not contain in their own genome all the genes required to run through the entire life cycle. Such viruses are dependent on various helper functions that have to be provided by other viruses but are nevertheless known as "viruses" to a person skilled in the art. For example, the Hepatitis Delta Virus (HDV) needs the help of Hepatitis B Virus (HBV), or the satellite virus of the "Maize White Line Mosaic Virus" needs the help of the "Maize White Line Mosaic Virus" to run

through its life cycle. Consequently, the amplicon in D1 can also be regarded as a virus or helper virus.

The amplicon is used in D1 as a helper virus for producing infectious AAV vector preparations. The method comprises the introduction by infection of the recombinant AAV vector and recombinant helper virus into HeLa cells (page 8786, right-hand column, lines 21-37), yielding cells which contain both vectors and from which an infectious AAV preparation is extracted (page 8786, right-hand column, lines 21-37, and page 8788, left-hand column, lines 42-44). Consequently, the technical features of the method disclosed in D1 for producing recombinant AA viruses are identical to the features of the method which constitutes the subject matter of Claim 28. Consequently, Claim 28 is not novel and not inventive (PCT Article 33(2) and (3)).

VIII. Certain observations on the international application

The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:

Claims 2-10 do not meet the requirements of PCT Article 6 because the subject matter for which protection is sought is not clearly defined. These claims attempt to define their subject matter in terms of the result to be achieved, and in doing so merely state the problem addressed. Consequently, it is unclear how a person skilled in the art inserts the rep and cap genes in a stable manner and produces the virus which does not undergo reversion. It is pointed out to the applicants that it is clear to a person skilled in the art how to check virus stability. However, it is not clear what technical features need to be considered in order to produce a stable recombinant virus which does not undergo reversion.

PATENT COOPERATION TREATY

From the INTERNATIONAL BUREAU

PCT

NOTIFICATION OF TRANSMITTAL OF COPIES OF TRANSLATION OF THE INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Rule 72.2)

To:

WEICKMANN, H.
Kopernikusstrasse 9
D-81679 München
ALLEMAGNE

Date of mailing (day/month/year) 06 February 2001 (06.02.01)	
Applicant's or agent's file reference 18397P WO	IMPORTANT NOTIFICATION
International application No. PCT/EP98/05542	International filing date (day/month/year) 01 September 1998 (01.09.98)
Applicant HEILBRONN, Regine et al	

1. Transmittal of the translation to the applicant.

The International Bureau transmits herewith a copy of the English translation made by the International Bureau of the international preliminary examination report established by the International Preliminary Examining Authority.

2. Transmittal of the copy of the translation to the elected Offices.

The International Bureau notifies the applicant that copies of that translation have been transmitted to the following elected Offices requiring such translation:

CA,JP,US

The following elected Offices, having waived the requirement for such a transmittal at this time, will receive copies of that translation from the International Bureau only upon their request:

EP,IL

3. Reminder regarding translation into (one of) the official language(s) of the elected Office(s).

The applicant is reminded that, where a translation of the international application must be furnished to an elected Office, that translation must contain a translation of any annexes to the international preliminary examination report.

It is the applicant's responsibility to prepare and furnish such translation directly to each elected Office concerned (Rule 74.1). See Volume II of the PCT Applicant's Guide for further details.

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No. (41-22) 740.14.35

Authorized officer

Claudio Borton

Telephone No. (41-22) 338.83.38

Translation

PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 18397P WO	FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/EP98/05542	International filing date (day/month/year) 01 September 1998 (01.09.98)	Priority date (day month year) 06 July 1998 (06.07.98)
International Patent Classification (IPC) or national classification and IPC C12N 15/86, 7/01, 7/04, 5/10		
Applicant HEILBRONN, Regine		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.

2. This REPORT consists of a total of 7 sheets, including this cover sheet.

☒ This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

These annexes consist of a total of 1 sheets.

3. This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☐ Non-establishment of opinion with regard to novelty, inventive step and industrial applicability
- IV ☐ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☐ Certain documents cited
- VII ☐ Certain defects in the international application
- VIII ☒ Certain observations on the international application

Date of submission of the demand	Date of completion of this report
04 February 2000 (04.02.00)	28 December 2000 (28.12.2000)
Name and mailing address of the IPEA/EP Facsimile No.	Authorized officer Telephone No.

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No.
PCT/EP98/05542

I. Basis of the report

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Nos. _____ . filed with the demand.
Nos. 1,14 . filed with the letter of 16 October 2000 (16.10.2000) .
Nos. _____ . filed with the letter of _____ .

☒ the drawings. sheets/fig 1/5-5/5 . as originally filed.
sheets/fig _____ . filed with the demand.
sheets/fig _____ . filed with the letter of _____ .
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2. The amendments have resulted in the cancellation of:

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☐ the claims. Nos. _____
☐ the drawings. sheets/fig _____

3. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the Supplemental Box (Rule 70.2(c)).

4. Additional observations, if necessary:

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No.
PCT/EP 98/05542

V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. Statement

Novelty (N)	Claims	1-27	YES
	Claims	28	NO
Inventive step (IS)	Claims	1-27	YES
	Claims	28	NO
Industrial applicability (IA)	Claims	1-28	YES
	Claims		NO

2. Citations and explanations

This application concerns a recombinant herpes virus and a method for producing the same. The herpes virus also serves as helper virus when producing recombinant adeno-associated viruses (AAV) designed for use in research and therapy. Other claims are directed to corresponding cells and nucleic acids.

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D1: CONWAY ET AL.: "Recombinant adeno-associated virus type 2 replication and packaging is entirely supported by *herpes simplex* virus type 1 amplicon expressing rep and cap", JOURNAL OF VIROLOGY, Vol. 71, No. 11, November 1997.

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restriction cleavage of a fragment that codes for a rep and cap gene, then ligation with a viral vector with a singular *XbaI* restriction site (page 8781, right-hand column, lines 25-56). The singular *XbaI* restriction site in the viral vector of D1 connects the HSV genomic DNA fragment with the DNA of the pUC-based vector. Consequently, it is assumed that the insertion of the fragment coding for the rep and cap genes described in D1 is not integrated in the genome of the herpes virus, but rather that the fragments coding for the rep and cap genes are inserted beside the HSV genomic fragment. Since the method of the present Claims 10-13, the recombinant HSV as per Claims 1-9, the nucleic acid as per Claim 14 and the vector as per Claim 15 are characterised in that the rep and cap genes are located on an insertion inserted in the genome of the herpes virus (and not beside the genomic fragment of the herpes virus), the method and DNA construct of D1 differ from the method and DNA construct of the present application, and Claims 1-15 should therefore be considered novel (PCT Article 33(2)).

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recombinant HSV as per Claims 1-3 and are therefore characterised by the same advantage, that is, the thus produced recombinant HSV is free from wild type herpes virus. Claims 1-15 should therefore be considered inventive (PCT Article 33(3)).

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The following observations on the clarity of the claims, description, and drawings or on the question whether the claims are fully supported by the description, are made:

Claims 2-10 do not meet the requirements of PCT Article 6 because the subject matter for which protection is sought is not clearly defined. These claims attempt to define their subject matter in terms of the result to be achieved, and in doing so merely state the problem addressed. Consequently, it is unclear how a person skilled in the art inserts the rep and cap genes in a stable manner and produces the virus which does not undergo reversion. It is pointed out to the applicants that it is clear to a person skilled in the art how to check virus stability. However, it is not clear what technical features need to be considered in order to produce a stable recombinant virus which does not undergo reversion.

00/72252 5630

VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES PATENTWESENS

PCT

INTERNATIONALER VORLÄUFIGER PRÜFUNGSBERICHT

(Artikel 36 und Regel 70 PCT)

T6

Aktenzeichen des Anmelders oder Anwalts	WEITERES VORGEHEN	siehe Mitteilung über die Übersendung des internationalen vorläufigen Prüfungsberichts (Formblatt PCT/IPEA/416)
18397P WO		
Internationales Aktenzeichen	Internationales Anmeldedatum *(Tag/Monat/Jahr)*	Prioritätsdatum *(Tag/Monat/Tag)*
PCT/EP98/05542	01/09/1998	06/07/1998

Internationale Patentklassifikation (IPK) oder nationale Klassifikation und IPK
C12N15/86

Anmelder
HEILBRONN, Regine et al.

1. Dieser internationale vorläufige Prüfungsbericht wurde von der mit der internationalen vorläufigen Prüfung beauftragten Behörde erstellt und wird dem Anmelder gemäß Artikel 36 übermittelt.

2. Dieser BERICHT umfaßt insgesamt 7 Blätter einschließlich dieses Deckblatts.

   ☒ Außerdem liegen dem Bericht ANLAGEN bei; dabei handelt es sich um Blätter mit Beschreibungen, Ansprüchen und/oder Zeichnungen, die geändert wurden und diesem Bericht zugrunde liegen, und/oder Blätter mit vor dieser Behörde vorgenommenen Berichtigungen (siehe Regel 70.16 und Abschnitt 607 der Verwaltungsrichtlinien zum PCT).

   Diese Anlagen umfassen insgesamt 1 Blätter.

3. Dieser Bericht enthält Angaben zu folgenden Punkten:

   - I ☒ Grundlage des Berichts
   - II ☐ Priorität
   - III ☐ Keine Erstellung eines Gutachtens über Neuheit, erfinderische Tätigkeit und gewerbliche Anwendbarkeit
   - IV ☐ Mangelnde Einheitlichkeit der Erfindung
   - V ☒ Begründete Feststellung nach Artikel 35(2) hinsichtlich der Neuheit, der erfinderischen Tätigkeit und der gewerblichen Anwendbarkeit; Unterlagen und Erklärungen zur Stützung dieser Feststellung
   - VI ☐ Bestimmte angeführte Unterlagen
   - VII ☐ Bestimmte Mängel der internationalen Anmeldung
   - VIII ☒ Bestimmte Bemerkungen zur internationalen Anmeldung

Datum der Einreichung des Antrags	Datum der Fertigstellung dieses Berichts
04/02/2000	28.12.2000

Name und Postanschrift der mit der internationalen vorläufigen Prüfung beauftragten Behörde:
Europäisches Patentamt
D-80298 München
Tel. +49 89 2399 - 0 Tx: 523656 epmu d
Fax: +49 89 2399 - 4465

Bevollmächtigter Bediensteter
Celler, J
Tel. Nr. +49 89 2399 7336

INTERNATIONALER VORLÄUFIGER PRÜFUNGSBERICHT

Internationales Aktenzeichen PCT/EP98/05542

I. Grundlage des Berichts

1. Dieser Bericht wurde erstellt auf der Grundlage (*Ersatzblätter, die dem Anmeldeamt auf eine Aufforderung nach Artikel 14 hin vorgelegt wurden, gelten im Rahmen dieses Berichts als "ursprünglich eingereicht" und sind ihm nicht beigefügt, weil sie keine Änderungen enthalten.*):
Beschreibung, Seiten:

1-29	ursprüngliche Fassung	

Patentansprüche, Nr.:

2-13,15-28	ursprüngliche Fassung	
1,14	mit Telefax vom	16/10/2000

Zeichnungen, Blätter:

1/5-5/5	ursprüngliche Fassung	

2. Hinsichtlich der **Sprache**: Alle vorstehend genannten Bestandteile standen der Behörde in der Sprache, in der die internationale Anmeldung eingereicht worden ist, zur Verfügung oder wurden in dieser eingereicht, sofern unter diesem Punkt nichts anderes angegeben ist.

   Die Bestandteile standen der Behörde in der Sprache: zur Verfügung bzw. wurden in dieser Sprache eingereicht; dabei handelt es sich um

   ☐ die Sprache der Übersetzung, die für die Zwecke der internationalen Recherche eingereicht worden ist (nach Regel 23.1(b)).

   ☐ die Veröffentlichungssprache der internationalen Anmeldung (nach Regel 48.3(b)).

   ☐ die Sprache der Übersetzung, die für die Zwecke der internationalen vorläufigen Prüfung eingereicht worden ist (nach Regel 55.2 und/oder 55.3).

3. Hinsichtlich der in der internationalen Anmeldung offenbarten **Nucleotid- und/oder Aminosäuresequenz** ist die internationale vorläufige Prüfung auf der Grundlage des Sequenzprotokolls durchgeführt worden, das:

   ☐ in der internationalen Anmeldung in schriftlicher Form enthalten ist.

   ☐ zusammen mit der internationalen Anmeldung in computerlesbarer Form eingereicht worden ist.

   ☐ bei der Behörde nachträglich in schriftlicher Form eingereicht worden ist.

   ☐ bei der Behörde nachträglich in computerlesbarer Form eingereicht worden ist.

   ☐ Die Erklärung, daß das nachträglich eingereichte schriftliche Sequenzprotokoll nicht über den Offenbarungsgehalt der internationalen Anmeldung im Anmeldezeitpunkt hinausgeht, wurde vorgelegt.

   ☐ Die Erklärung, daß die in computerlesbarer Form erfassten Informationen dem schriftlichen Sequenzprotokoll entsprechen, wurde vorgelegt.

4. Aufgrund der Änderungen sind folgende Unterlagen fortgefallen:

   ☐ Beschreibung, Seiten:
   ☐ Ansprüche, Nr.:
   ☐ Zeichnungen, Blatt:

5. ☐ Dieser Bericht ist ohne Berücksichtigung (von einigen) der Änderungen erstellt worden, da diese aus den angegebenen Gründen nach Auffassung der Behörde über den Offenbarungsgehalt in der ursprünglich eingereichten Fassung hinausgehen (Regel 70.2(c)).

   (Auf Ersatzblätter, die solche Änderungen enthalten, ist unter Punkt 1 hinzuweisen;sie sind diesem Bericht beizufügen).

6. Etwaige zusätzliche Bemerkungen:

V. Begründete Feststellung nach Artikel 35(2) hinsichtlich der Neuheit, der erfinderischen Tätigkeit und der gewerblichen Anwendbarkeit; Unterlagen und Erklärungen zur Stützung dieser Feststellung

1. Feststellung

Neuheit (N)	Ja:	Ansprüche	1 - 27
	Nein:	Ansprüche	28
Erfinderische Tätigkeit (ET)	Ja:	Ansprüche	1 - 27
	Nein:	Ansprüche	28
Gewerbliche Anwendbarkeit (GA)	Ja:	Ansprüche	1 - 28
	Nein:	Ansprüche	

2. Unterlagen und Erklärungen
   siehe Beiblatt

VIII. Bestimmte Bemerkungen zur internationalen Anmeldung

Zur Klarheit der Patentansprüche, der Beschreibung und der Zeichnungen oder zu der Frage, ob die Ansprüche in vollem Umfang durch die Beschreibung gestützt werden, ist folgendes zu bemerken:
siehe Beiblatt

Zu Punkt V

Begründete Feststellung nach Artikel 35(2) hinsichtlich der Neuheit, der erfinderischen Tätigkeit und der gewerblichen Anwendbarkeit; Unterlagen und Erklärungen zur Stützung dieser Feststellung

Diese Anmeldung bezieht sich auf ein rekombinantes Herpesvirus und ein Verfahren zu dessen Herstellung. Das Herpesvirus dient weiter als ein Helfervirus bei der Herstellung rekombinanter Adeno-assoziierten Viren (AAV), die für Einsatz in Forschung und Therapie gedacht sind. Weitere Ansprüche sind auf entsprechende Zellen und Nukleinsäuren gerichtet.

Es wird auf die folgenden Dokumente verwiesen:

D1: CONWAY ET AL.: "Recombinant adeno-associated virus type 2 replicaltion and packaging is entirely supported by herpes simplex virus type 1 amplicon expressing rep and cap" JOURNAL OF VIROLOGY, Bd. 71, Nr. 11, November 1997

1. D1 beschreibt ein Verfahren zur Herstellung eines rekombinanten Herpes-Simplex-Virus Typ 1 Amplikons. Ein DNS-Konstrukt wurde hergestellt, das die zur Replikation von AAV erforderlichen Helferfunktionen eines Herpersvirusgenoms und darin inseriert ein rep- und cap-Gen von AAV jeweils in operativer Verknüpfung mit ihrer nativen Expressionskontrollsequenz umfaßt (z. B. Seite 8781, rechte Spalte, Zeile 25 - 56 und Seite 8780, Zeile 17 - 25). Die Konstruktion erfolgte durch *Xbal*-Restriktionspaltung eines rep- und cap-Gen kodierenden Fragmentes und folgende Ligation mit einem viralen Vektor, der eine singuläre *Xbal*-Restriktionstelle hat (Seite 8781, rechte Spalte, Zeile 25 - 56). Die singuläre *Xbal*-Restriktionstelle in dem viralen Vektor von D1 verbindet das HSV-genomische DNS-Fragment mit der DNS des pUC-basierenden Vektors. Daher wird davon ausgegangen, daß die in D1 beschriebene Insertion des rep- und cap-Gen kodierenden Fragmentes nicht im Genom des Herpesvirus integriert ist

sondern das rep- und cap-Gen kodierenden Fragmente neben dem HSV-genomischen Fragment inseriert ist. Da das Verfahren der vorliegenden Ansprüche 10 - 13, das rekombinante HSV der Ansprüche 1 - 9, die Nukleinsäure des Anspruchs 14 und der Vektor des Anspruchs 15 dadurch gekennzeichnet sind, daß das rep- und cap-Gen sich auf einer Insertion befinden, die im Genom des Herpesvirus (und nicht neben dem genomischen Fragment des Herpesvirus) inseriert ist, unterscheidet sich das in D1 offenbarte Verfahren und das DNS-Konstrukt von dem Verfahren und dem DNS-Konstrukt der vorliegenden Anmeldung und daher sind die Ansprüche 1 - 15 als neu anzusehen (Art. 33(2) PCT).

2. Darüberhinaus zeigt die Analyse in D1, daß die virale Zusammensetzung neben dem rekombinanten Virus - HSV-RC/*d27*, auch Wildtyp-Herpesvirus enthält (Seite 8782, linke Spalte, Zeilen 27 - 39). Dagegen ist das rekombinante HSV der vorliegenden Ansprüche 1 - 9 Wildtyp-Herpesvirus frei und homogen. Daher sind, zum Beispiel, die Mengen des rekombinanten HSV der vorliegenden Anmeldung einfacher zu bestimmen und besser kontrollierbar gegenüber denen von D1. Die Nukleinsäure des Anspruchs 14 und der Vektor des Anspruchs 15, die im Verfahren der Ansprüche 10 -13 verwendbar sind, dienen der Herstellung der rekombinanten HSV nach Ansprüchen 1 - 9 und sind damit durch den selben Vorteil gekennzeichnet, i.e. das hergestellte, rekombinante HSV ist Wildtyp-Herpesvirus frei. Somit sind die Ansprüche 1 - 15 als erfinderisch anzusehen (Art. 33(3) PCT).

3. Da die Ansprüche 16 - 27 entweder direkt oder indirekt von Ansprüchen 1- 9 abhängen, sind die Ansprüche 16 - 27 ebenfalls als neu und erfinderisch anzusehen (Art. 33(2) und (3) PCT).

4. Hinsichtlich des unabhängigen Anspruchs 28 wird der Anmelder darauf hingewiesen, daß das rekombinante Herpes-Simplex-Virus Typ 1 Amplikon von D1 mit Einsatz eines Helfervirus in infektöse Hüllen verpackt werden kann. Da auf diese Weise das Amplikon einen kompleten Lebenszyklus eines Virus, i. e. Vermehrung, Verpackung und Infektion, durchlaufen kann, kann das Amplikon als Virus gesehen werden. Der Begriff "Virus" hat sehr großen Umfang für einen Fachmann. Ein Virus kann DNS oder RNS enthalten, kann tierische, menschliche

als auch pflanzliche Zellen zur Vermehrung benötigen. Die Frage, ob Phagen, die bakterielle Zellen als Wirt nutzen zu den Viren zu zählen sind, kann nicht eindeutig beantwortet werden. Weiterhin, sind im Stand der Technik "Viren" beschrieben, die in ihrem eigenen Genom nicht alle Gene haben, die für das Durchlaufen des kompletten Lebenszyklus notwendig sind. Solche Viren sind abhängig von verschiedenen Helferfunktionen, die von den anderen Viren bereitgestellt werden müssen, sie sind aber trotzdem, für den Fachmann unter dem Begriff "Virus" bekannt. Zum Beispiel, Hepatitis Delta Virus (HDV), das auf die Hilfe vom Hepatitis B Virus (HBV) angewiesen ist oder Satellitvirus des "Maize White Line Mosaic Virus", dessen Lebenszyklus auf der Hilfe von "Maize White Line Mosaic Virus" beruht. Daher kann das Amplikon von D1 auch als Virus, beziehungsweise Helfervirus angesehen werden.

Das Amplikon wird in D1 zur Produktion von infektiösen AAV-Vektorpräparationen als Helfervirus eingesetzt. Das Verfahren umfaßt das Einbringen des rekombinanten AAV-Vektors und des rekombinanten Helfervirus durch Infektion in HeLa-Zellen (Seite 8786, rechte Spalte, Zeilen 21 - 37). Dadurch entstehen Zellen, die beide Vektoren enthalten und aus denen eine infektiöse AAV-Präparation gewonnen wird (Seite 8786, rechte Spalte, Zeilen 21 - 37 und Seite 8788, linke Spalte, Zeilen 42 - 44). Somit sind die technischen Merkmale des in D1 offenbarten Verfahrens zur Herstellung rekombinanter AA-Viren identisch mit den Merkmalen des Verfahrens, das den Gegenstand des Anspruchs 28 darstellt. Demzufolge ist der Anspruch 28 nicht neu und nicht erfinderisch (Art. 33(2) und (3) PCT).

Zu Punkt VIII

Bestimmte Bemerkungen zur internationalen Anmeldung

Ansprüche 2 und 10 entsprechen nicht den Erfordernissen des Art. 6 PCT, weil der Gegenstand des Schutzbegehrens nicht klar definiert ist. In den Ansprüchen wird versucht, den Gegenstand durch das zu erreichende Ergebnis zu definieren; damit wird aber lediglich die zu lösende Aufgabe angegeben. Deswegen ist es

unklar wie ein Fachmann die rep- und cap-Gene stabil inseriert und das Virus, das keine Reversion zeigt, herstellen soll. Der Anmelder wird darauf hingewiesen, daß einem Fachmann klar ist, wie man die Virusstabilität überprüft. Es ist jedoch unklar, welche technischen Merkmale berücksichtigt werden müssen um ein stabiles, rekombinantes Virus, das keine Reversion zeigt, herzustellen.

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PCT/EP98/05542
Prof. Dr. Regine Heilbronn

Neue Ansprüche

1. Rekombinantes Herpesvirus,
dadurch gekennzeichnet,
dass es ein rep- und ein cap-Gen von Adeno-assoziierten Viren (AAV) in operativer Verknüpfung mit einer Expressionskontrollsequenz enthält, wobei sich das rep- und das cap-Gen auf einer Insertion befinden, die im Genom des Herpesvirus integriert ist.

14. Nukleinsäure umfassend die zur Replikation von AAV-Viren erforderlichen Helferfunktionen eines Herpesvirusgenoms und darin insertiert ein rep- und ein cap-Gen von Adeno-assoziierten Viren (AAV) jeweils in operativer Verknüpfung einer Expressionskontrollsequenz, wobei sich das rep- und das cap-Gen auf einer Insertion befinden, die im Genom des Herpesvirus integriert ist.

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Feld Nr. VI PRIORITÄTSANSPRUCH

☐ Weitere Prioritätsansprüche sind im Zusatzfeld angegeben.

	Anmeldedatum der früheren Anmeldung (Tag/Monat)	Aktenzeichen der früheren Anmeldung	Ist die frühere Anmeldung eine: national Anmeldung: Staat	regionale Anmeldung:* regionales Amt	internationale Anmeldung: Anmeldeamt
Zeile (1)	(06. 07. 98) 06.Juli 1998	198 30 141.3	DE		
Zeile (2)					
Zeile (3)					

☐ Das Anmeldeamt wird ersucht, eine beglaubigte Abschrift der oben in der (den) Zeile(n) _____ bezeichneten früheren Anmeldung(en) zu erstellen und dem internationalen Büro zu übermitteln *(nur falls die frühere Anmeldung(en) bei dem Amt eingereicht worden ist(sind), das für die Zwecke dieser internationalen Anmeldung Anmeldeamt ist)*

* *Falls es sich bei der früheren Anmeldung um eine ARIPO-Anmeldung handelt, so muß in dem Zusatzfeld mindestens ein Staat angegeben werden, der Mitgliedstaat der Pariser Verbandsübereinkunft zum Schutz des gewerblichen Eigentums ist und für den die frühere Anmeldung eingereicht wurde.*

Feld Nr. VII INTERNATIONALE RECHERCHENBEHÖRDE

Wahl der internationalen Recherchenbehörde (ISA) *(falls zwei oder mehr als zwei internationale Recherchenbehörden für die Ausführung der internationalen Recherche zuständig sind, geben Sie die von Ihnen gewählte Behörde an; der Zweibuchstaben-Code kann benutzt werden)*

ISA /

Antrag auf Nutzung der Ergebnisse einer früheren Recherche: Bezugnahme auf diese frühere Recherche *(falls eine frühere Recherche bei der internationalen Recherchenbehörde beantragt oder von ihr durchgeführt worden ist):*

Datum *(Tag/Monat/Jahr)* Aktenzeichen Staat *(oder regionales Amt)*

Feld Nr. VIII KONTROLLISTE; EINREICHUNGSSPRACHE

Diese internationale Anmeldung enthält die folgende Anzahl von Blättern:

Antrag	:	3
Beschreibung (ohne Sequenzprotokollteil)	:	29
Ansprüche	:	5
Zusammenfassung	:	1
Zeichnungen	:	5
Sequenzprotokollteil der Beschreibung	:	
Blattzahl insgesamt	:	43

Dieser internationalen Anmeldung liegen die nachstehend angekreuzten Unterlagen bei:

1. ☒ Blatt für die Gebührenberechnung
2. ☐ Gesonderte unterzeichnete Vollmacht
3. ☐ Kopie der allgemeinen Vollmacht: Aktenzeichen (falls vorhanden):
4. ☐ Begründung für das Fehlen einer Unterschrift
5. ☐ Prioritätsbeleg(e), in Feld Nr. VI durch folgende Zeilennummer gekennzeichnet:
6. ☐ Übersetzung der internationalen Anmeldung in die folgende Sprache:
7. ☐ Gesonderte Angaben zu hinterlegten Mikroorganismen oder anderem biologischen Material
8. ☐ Sequenzprotokolle für Nucleotide und/oder Aminosäuren in computerlesbarer Form
9. ☐ Sonstige *(einzeln aufführen)*:

Abbildung der Zeichnungen, die mit der Zusammenfassung veröffentlicht werden soll (Nr.):

Sprache, in der die internationale Anmeldung eingereicht wird: DE

Feld Nr. IX UNTERSCHRIFT DES ANMELDERS ODER DES ANWALTS

Der Name jeder unterzeichnenden Person ist neben der Unterschrift zu wiederholen, und es ist anzugeben, sofern sich dies nicht eindeutig aus dem Antrag ergibt, in welcher Eigenschaft die Person unterzeichnet.

B. Böhm

Dipl.-Chem. Dr. B. Böhm

Vom Anmeldeamt auszufüllen

1. Datum des tatsächlichen Eingangs dieser internationalen Anmeldung: 01 SEP 1998 (= 1. 09. 98)

2. Zeichnungen ☒ eingegangen: ☐ nicht eingegangen:

3. Geändertes Eingangsdatum aufgrund nachträglich, jedoch fristgerecht eingegangener Unterlagen oder Zeichnungen zur Vervollständigung dieser internationalen Anmeldung:

4. Datum des fristgerechten Eingangs der angeforderten Richtigstellungen nach Artikel 11(2) PCT:

5. Internationale Recherchenbehörde *(falls zwei oder mehr zuständig sind)*: ISA /

6. ☐ Übermittlung des Recherchenexemplars bis zur Zahlung der Recherchengebühr aufgeschoben

Vom Internationalen Büro auszufüllen

Datum des Eingangs des Aktenexemplars beim Internationalen Büro:

PCT/EP 98 / 05542

Feld Nr. V BESTIMMUNG VON STAATEN

Die folgenden Bestimmungen nach Regel 4.9 Absatz a werden hiermit vorgenommen *(bitte die entsprechenden Kästchen ankreuzen; wenigstens ein Kästchen muß angekreuzt werden)*:

Regionales Patent

- ☐ AP ARIPO-Patent: GH Ghana, GM Gambia, KE Kenia, LS Lesotho, MW Malawi, SD Sudan, SZ Swasiland, UG Uganda, ZW Simbabwe und jeder weitere Staat, der Vertragsstaat des Harare-Protokolls und des PCT ist
- ☐ EA Eurasisches Patent: AM Armenien, AZ Aserbaidschan, BY Belarus, KG Kirgisistan, KZ Kasachstan, MD Republik Moldau, RU Russische Föderation, TJ Tadschikistan, TM Turkmenistan und jeder weitere Staat, der Vertragsstaat des Eurasischen Patentübereinkommens und des PCT ist
- ☒ EP Europäisches Patent: AT Österreich, BE Belgien, CH und LI Schweiz und Liechtenstein, CY Zypern, DE Deutschland, DK Dänemark, ES Spanien, FI Finnland, FR Frankreich, GB Vereinigtes Königreich, GR Griechenland, IE Irland, IT Italien, LU Luxemburg, MC Monaco, NL Niederlande, PT Portugal, SE Schweden und jeder weitere Staat, der Vertragsstaat des Europäischen Patentübereinkommens und des PCT ist
- ☐ OA OAPI-Patent: BF Burkina Faso, BJ Benin, CF Zentralafrikanische Republik, CG Kongo, CI Côte d'Ivoire, CM Kamerun, GA Gabun, GN Guinea, ML Mali, MR Mauretanien, NE Niger, SN Senegal, TD Tschad, TG Togo und jeder weitere Staat, der Vertragsstaat der OAPI und des PCT ist *(falls eine andere Schutzrechtsart oder ein sonstiges Verfahren gewünscht wird, bitte auf der gepunkteten Linie angeben)* .....

Nationales Patent *(falls eine andere Schutzrechtsart oder ein sonstiges Verfahren gewünscht wird, bitte auf der gepunkteten Linie angeben)*:

- ☐ AL Albanien
- ☐ AM Armenien
- ☐ AT Österreich
- ☐ AU Australien
- ☐ AZ Aserbaidschan
- ☐ BA Bosnien-Herzegowina
- ☐ BB Barbados
- ☐ BG Bulgarien
- ☐ BR Brasilien
- ☐ BY Belarus
- ☒ CA Kanada
- ☐ CH und LI Schweiz und Liechtenstein
- ☐ CN China
- ☐ CU Kuba
- ☐ CZ Tschechische Republik
- ☐ DE Deutschland
- ☐ DK Dänemark
- ☐ EE Estland
- ☐ ES Spanien
- ☐ FI Finnland
- ☐ GB Vereinigtes Königreich
- ☐ GE Georgien
- ☐ GH Ghana
- ☐ GM Gambia
- ☐ ~~GW Guinea-Bissau~~
- ☐ HR Kroatien
- ☐ HU Ungarn
- ☐ ID Indonesien
- ☒ IL Israel
- ☐ IS Island
- ☒ JP Japan
- ☐ KE Kenia
- ☐ KG Kirgisistan
- ☐ KP Demokratische Volksrepublik Korea
- ☐ .....
- ☐ KR Republik Korea
- ☐ KZ Kasachstan
- ☐ LC Saint Lucia
- ☐ LK Sri Lanka
- ☐ LR Liberia
- ☐ LS Lesotho
- ☐ LT Litauen
- ☐ LU Luxemburg
- ☐ LV Lettland
- ☐ MD Republik Moldau
- ☐ MG Madagaskar
- ☐ MK Die ehemalige jugoslawische Republik Mazedonien
- ☐ MN Mongolei
- ☐ MW Malawi
- ☐ MX Mexiko
- ☐ NO Norwegen
- ☐ NZ Neuseeland
- ☐ PL Polen
- ☐ PT Portugal
- ☐ RO Rumänien
- ☐ RU Russische Föderation
- ☐ SD Sudan
- ☐ SE Schweden
- ☐ SG Singapur
- ☐ SI Slowenien
- ☐ SK Slowakei
- ☐ SL Sierra Leone
- ☐ TJ Tadschikistan
- ☐ TM Turkmenistan
- ☐ TR Türkei
- ☐ TT Trinidad und Tobago
- ☐ UA Ukraine
- ☐ UG Uganda
- ☒ US Vereinigte Staaten von Amerika
- ☐ UZ Usbekistan
- ☐ VN Vietnam
- ☐ YU Jugoslawien
- ☐ ZW Simbabwe

Kästchen für die Bestimmung von Staaten (für die Zwecke eines nationalen Patents), die dem PCT nach der Veröffentlichung dieses Formblatts beigetreten sind:

- ☐ .....
- ☐ .....

Erklärung bzgl. vorsorglicher Bestimmungen: Zusätzlich zu den oben genannten Bestimmungen nimmt der Anmelder nach Regel 4.9 Absatz b auch alle anderen nach dem PCT zulässigen Bestimmungen vor mit Ausnahme der im Zusatzfeld genannten Bestimmungen, die von dieser Erklärung ausgenommen sind. Der Anmelder erklärt, daß diese zusätzlichen Bestimmungen unter dem Vorbehalt einer Bestätigung stehen und jede zusätzliche Bestimmung, die vor Ablauf von 15 Monaten ab dem Prioritätsdatum nicht bestätigt wurde, nach Ablauf dieser Frist als vom Anmelder zurückgenommen gilt. *(Die Bestätigung einer Bestimmung erfolgt durch die Einreichung einer Mitteilung, in der diese Bestimmung angegeben wird, und die Zahlung der Bestimmungs- und der Bestätigungsgebühr. Die Bestätigung muß beim Anmeldeamt innerhalb der Frist von 15 Monaten eingehen.)*